



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 141622

TO: Bennett Celsa
Location: rem/2a25/2a05
Art Unit: 1639
Thursday, January 06, 2005

Case Serial Number: 09/748739

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

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Need
by

1/12/05

Access DB# 141622

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: BENNETT CELSA Examiner #: 73815 Date: 1/13/05
Art Unit: 1639 Phone Number 301-272-0807 Serial Number: 091748739
Mail Box and Bldg/Room Location: 571 Results Format Preferred (circle): PAPER DISKET MAIL

2A05

REMSEN
2A35

2A25

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: BUTYRCHOLINE esterase variants

Inventors (please provide full names): LOCKRIDGE WATKINS

See
attached
B2B

Earliest Priority Filing Date: 12/26/00

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please
IN RELEVANT DATABASES: (see claim 1)

1. SEQ search of:

≥ 95% Identity to 1-602 of seq 2
AND aa-602 m

≥ 95% Identity to 29-602 of seq 2

NOTE FYI: TRP must be present AT
Position 356 (NOT 328) of seq 2

2. PERCEPION INTERFERENCE search
for above

Attached
1. B2B
2. Claims 1-2

Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
GMT 0A02 Tel: 308-4491

P.U. 1-6-05
S.D. 1-6-05

thanks

EX CELSA - 20807

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:27:17 ; Search time 197 seconds

(without alignments)
1758.251 Million cell updates/sec

Title: US-09-748-739A-2

Perfect score: 3260
Sequence: 1 MDSKVITICIRFLFWPLL.C.....MDMKQFNQDYTSKKSCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3239	99.4	602	1	CHLE_HUMAN
2	2858	87.7	602	1	Q9NIN9
3	2855.5	87.6	581	1	CHLE_RABIT
4	2784	85.4	602	1	CHLE_FELCA
5	2774	85.1	574	1	CHLE_HORSE
6	2772	85.0	602	1	CHLE_PANTT
7	2602	79.8	603	2	BAC34196
8	2593	79.5	603	1	CHLE_MOUSE
9	2588	79.4	597	2	Q9JKT1
10	2339.5	71.8	603	2	Q90ZK8
11	1777	54.5	633	1	ACES_EBEL
12	1766.5	54.2	634	1	ACES_BRABE
13	1730.5	53.1	606	1	ACES_BUNFA
14	1698.5	52.1	614	1	ACES_HUMAN
15	1698.5	52.1	614	2	AP23465
16	1693.5	51.9	614	1	ACES_RAT
17	1692.5	51.9	614	1	ACES_MOUSE
18	1692.5	51.9	614	2	BAC31228
19	1692.5	51.9	614	2	BAC31641
20	1692.5	51.9	614	2	BAC32595
21	1683	51.6	611	1	ACES_FELCA
22	1674	51.3	349	2	Q9GKT6
23	1674	51.3	613	1	ACES_BOVIN
24	1654	50.7	586	1	ACES_TORCA
25	1654	50.7	590	1	ACES_TORNA
26	1649.5	50.6	584	1	ACES_RABIT
27	1567	48.1	617	2	Q86TM9
28	1466	45.0	767	2	ACES_CHICK
29	1449	44.4	602	2	Q76959
30	1390	42.6	605	2	Q76998
31	1367.5	41.9	526	2	Q86YX9

32	1324	40.6	701	2	Q75VX9	Q75VX9
33	1324	40.6	701	2	BAD06210	BAD06210
34	1317	40.4	702	1	ACES_CULPI	Q86GC8
35	1303	40.0	623	2	Q7RTM0	Q7RTM0
36	1303	40.0	737	1	ACE1_ANOGA	Q869C3
37	1303	40.0	743	2	Q7PUN2	Q7PUN2
38	1295	39.7	559	2	Q7PKM1	Q7PKM1
39	1295	39.7	687	2	Q86CZ4	Q86CZ4
40	1222.5	37.5	676	2	Q9BMJ1	Q9BMJ1
41	1218.5	37.4	660	2	Q6KAV3	Q6KAV3
42	1215.5	37.3	671	2	Q6KAV4	Q6KAV4
43	1214.5	37.3	676	2	Q6KAV5	Q6KAV5
44	1211.5	37.2	670	2	Q6KAV5	Q6KAV5
45	1206	37.0	610	2	Q9NHH6	Q9NHH6
46	1177.5	36.1	677	2	Q9NHH6	Q9NHH6
47	1172	36.0	656	2	Q96529	Q96529
48	1166	35.8	656	2	Q9XVX9	Q9XVX9
49	1153	35.4	620	1	ACE1_CABBR	Q27459
50	1152	35.3	638	2	Q86QW5	Q86QW5
51	1149	35.2	647	2	Q8MX85	Q86QW5
52	1142	35.0	620	1	ACES_LEPDE	P38433
53	1140.5	35.0	629	1	ACES_LEPDE	Q27677
54	1134	34.8	638	2	Q8MZL2	Q8MZL2
55	1127	34.6	585	2	Q7RTL6	Q7RTL6
56	1088.5	33.4	550	2	Q7RTL7	Q7RTL7
57	1079	33.1	587	2	Q6XR74	Q6XR74
58	1079	33.1	587	2	AP49302	AP49302
59	1079	33.1	593	2	Q6XR75	Q6XR75
60	1079	33.1	593	2	AP49301	AP49301
61	1075.5	33.0	637	2	Q9TX11	Q9TX11
62	1074.5	33.0	590	2	Q61987	Q61987
63	1069.5	32.8	596	2	Q6XR73	Q6XR73
64	1069.5	32.8	545	2	AP49303	AP49303
65	1063.5	32.6	645	2	Q7OR60	Q7OR60
66	1063.5	32.6	645	2	Q7RTI9	Q7RTI9
67	1059.5	32.5	664	1	ACES_ANOST	Q75VY0
68	1059.5	32.4	633	2	Q75VY0	Q75VY0
69	1055.5	32.4	692	2	BAD06209	BAD06209
70	1050	32.2	692	2	Q95P20	Q95P20
71	1050	32.2	692	2	Q95WV7	Q95WV7
72	1048	32.1	692	2	Q8MXC6	Q8MXC6
73	1048	32.1	692	2	Q8MXC8	Q8MXC8
74	1048	32.1	692	2	Q8MXC9	Q8MXC9
75	1047.5	32.1	595	2	Q45210	Q45210
76	1045	32.1	692	2	Q8MXC4	Q8MXC4
77	1044	32.0	649	1	ACES_DROME	Q7YZP7
78	1042.5	32.0	510	2	Q7YZP7	Q7YZP7
79	1042	32.0	691	2	Q8MXC5	Q8MXC5
80	1041.5	31.9	664	2	Q8TUV9	Q8TUV9
81	1041	31.9	692	2	Q8MXC7	Q8MXC7
82	1038.5	31.9	612	2	Q8MXC4	Q8MXC4
83	1033.5	31.7	604	1	ACE4_CABBR	Q9NDG8
84	1033	31.7	692	2	Q7YWD9	Q7YWD9
85	1029.5	31.6	708	2	P91954	P91954
86	1029	31.6	673	2	Q8MWZ4	Q8MWZ4
87	1028.5	31.5	603	2	Q7YZO0	Q7YZO0
88	1025.5	31.5	602	2	Q61372	Q61372
89	1025.5	31.5	528	2	Q62563	Q62563
90	1014.5	31.1	338	1	ACES_MXGL	Q92081
91	1014.5	31.1	664	2	Q8MW36	Q8MW36
92	1008	30.9	461	2	Q7YZP8	Q7YZP8
93	963.5	29.6	615	2	Q86GJ7	Q86GJ7
94	963	29.6	492	2	Q9GCP7	Q9GCP7
95	959	29.4	512	2	Q8MZM0	Q8MZM0
96	957.5	29.4	629	2	Q61378	Q61378
97	951	29.2	594	2	Q81T86	Q81T86
98	951	29.2	629	2	Q61371	Q61371
99	950.5	29.2	613	2	Q6XPY6	Q6XPY6
100	950.5	29.2	613	2	AA062949	AA062949

ALIGNMENTS

RESULT 1
CHIE_HUMAN STANDARD; PRT; 602 AA.
ID CHIE_HUMAN
AC P06276;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (choline esterase II) (Butyrylcholine esterase)
DE (pseudocholesterase).
GN Name=ACHE; Synonyms=CHE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=90212557; PubMed=2322535;
RA Appagou M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.,
RT "Structure of the gene for human butyrylcholinesterase. Evidence for a
RT single copy.";
RL Biochemistry 29:124-131(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87231856; PubMed=3035536;
RA Prody C.A., Zevin-Sonkin D., Gnat A., Goldberg O., Soreq H.,
RT "Isolation and characterization of full-length cDNA clones coding for
RT cholinesterase from fetal human tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88016155; PubMed=3477799;
RA McIernan C., Adkins S., Chaconnet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.,
RT "Brain cDNA clone for human cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uediri T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamarate P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Farey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 29-602.
RC TISSUE=Plasma;
RX MEDLINE=87109144; PubMed=3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.,
RT "Complete amino acid sequence of human serum cholinesterase.";
RL J. Biol. Chem. 262:549-557(1987).
RN [6]

RP DISULFIDE BONDS.
RX MEDLINE=88007487; PubMed=3115973;
RA Lockridge O., Adkins S., la Du B.N.,
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase.";
RL J. Biol. Chem. 262:12945-12952(1987).
RN [7]
RP REVIEW.
RX MEDLINE=89149758; PubMed=3067729;
RA Lockridge O.,
RT "Structure of human serum cholinesterase.";
RL Bioessays 9:125-128(1988).
RN [8]
RP VARIANT ATYPICAL GUY-98.
RX MEDLINE=89128896; PubMed=2915989;
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA van der Spek A.F.L., Lockridge O., la Du B.N.,
RT "Identification of the structural mutation responsible for the
RT dibucaine-resistant (atypical) variant form of human serum
RT cholinesterase.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [9]
RP VARIANT ILE-358.
RX MEDLINE=96287386; PubMed=8680411;
RA Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Moriwaiki K.,
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholinesterasemia.";
RL Hum. Mutat. 6:349-351(1995).
RN [10]
RP CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
RC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- DISASE: Mutant alleles of CHE1 are responsible for
CC hypocholinesterasemia resulting in suxamethonium sensitivity.
CC Homozygous persons sustain prolonged apnea after administration of
CC the muscle relaxant suxamethonium in connection with surgical
CC anesthesia.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
DR EMBL; M32391; AAA99296.1; -
DR EMBL; M32389; AAA99296.1; JOINED.
DR EMBL; M32390; AAA99296.1; JOINED.
DR EMBL; M15541; AAA98113.1; -
DR EMBL; M16474; AAA52015.1; -
DR EMBL; BC018141; AAH18141.1; -
DR PIR; A33769; ACNU.
DR PDB; 1EHO; Model; A=30-560.
DR PDB; 1EHO; Model; A=30-560.
DR PDB; 1P01; X-ray; A=29-557.
DR PDB; 1P0P; X-ray; A=29-557.
DR PDB; 1P0P; X-ray; A=29-557.
DR PDB; 1P0P; X-ray; A=29-557.
DR Genew; HGNC; 983; BCHE.
DR MIM; 177400; -
DR GO; GO:0001540; F:beta-amyloid binding; NAS.
DR GO; GO:0003824; F:catalytic activity; NAS.
DR GO; GO:0004104; F:cholinesterase activity; NAS.
DR GO; GO:0019899; F:enzyme binding; NAS.
DR GO; GO:0050783; P:cocaine metabolism; TAS.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.

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DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
KW 3D-structure; Direct protein sequencing; Disease mutation;
KW Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.
FT CHAIN 1 28
FT ACT_SITE 29 602 Cholinesterase.
FT ACT_SITE 353 353 Acyl-ester intermediate (By similarity).
FT ACT_SITE 466 466 Charge relay system (By similarity).
FT ACT_SITE 466 466 Charge relay system (By similarity).
FT DISULFID 93 120
FT DISULFID 280 291
FT DISULFID 428 547
FT DISULFID 599 599
FT CARBOHYD 45 45 Interchain.
FT CARBOHYD 85 85 N-linked (GlcNAc...).
FT CARBOHYD 134 134 N-linked (GlcNAc...).
FT CARBOHYD 269 269 N-linked (GlcNAc...).
FT CARBOHYD 284 284 N-linked (GlcNAc...).
FT CARBOHYD 369 369 N-linked (GlcNAc...).
FT CARBOHYD 483 483 N-linked (GlcNAc...).
FT CARBOHYD 509 509 N-linked (GlcNAc...).
FT CARBOHYD 514 514 N-linked (GlcNAc...).
FT CARBOHYD 98 98 D -> G (in atypical form, dibucaine-resistant; dbSNP:1799807).
FT VARIANT 98 98 /FTRD=VAR_002360.
FT VARIANT 271 271 T -> M (in fluoride-1).
FT VARIANT 271 271 /FTRD=VAR_002361.
FT VARIANT 358 358 L -> I (in hypocholinesterasemia).
FT VARIANT 418 418 G -> V (in fluoride-2).
FT VARIANT 567 567 A -> T (in K variant; with reduced enzyme activity; dbSNP:1803274).
FT VARIANT 567 567 /FTRD=VAR_002364.
SQ SEQUENCE 602 AA; 68418 MW; C9836405D9057F27 CRC64;

Query Match 99.4%; Score 3239; DB 1; Length 602;
Best Local Similarity 99.7%; Pred. No. 3,1e-23;
Matches 600; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKRGVGNLTVPFGTVAFLGIP 60
DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKRGVGNLTVPFGTVAFLGIP 60
QY 61 YAOPLGRRLRFFKKRQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120
DB 61 YAOPLGRRLRFFKKRQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120
QY 121 LYINWVLPAPKPKNAATVLMVYGGGQOTGSSLVYDGKFLARVERIYVSMYRVGALG 180
DB 121 LYINWVLPAPKPKNAATVLMVYGGGQOTGSSLVYDGKFLARVERIYVSMYRVGALG 180
QY 181 FLALPGNPEAPGNMGLFDQDLALOWVOKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
DB 181 FLALPGNPEAPGNMGLFDQDLALOWVOKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
QY 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKDPQEI 300
DB 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKDPQEI 300
QY 301 LLINEAFVYVPGTPLSVNFGPTVDGLTMDPDLLELQPKTKQIILGVNKKDEBTAAVY 360
DB 301 LLINEAFVYVPGTPLSVNFGPTVDGLTMDPDLLELQPKTKQIILGVNKKDEBTAAVY 360
QY 361 GAGPFSKDNNSITTRKFEQGLKIFPGVSEFGKESILFHYTPWVDORPENYREALGDV 420
DB 361 GAGPFSKDNNSITTRKFEQGLKIFPGVSEFGKESILFHYTPWVDORPENYREALGDV 420
QY 421 VGDYNPICPALPFTKSEWGNNAFFYYFEHRSSKLPWPMWGMGVEIEFVFGLEPLER 480
DB 421 VGDYNPICPALPFTKSEWGNNAFFYYFEHRSSKLPWPMWGMGVEIEFVFGLEPLER 480

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DB 421 VGDYNPICPALPFTKSEWGNNAFFYYFEHRSSKLPWPMWGMGVEIEFVFGLEPLER 480
QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTSWPVFKSTEOXYTLTINTESTRIMT 540
DB 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTSWPVFKSTEOXYTLTINTESTRIMT 540
QY 541 KLRAPQCRPMTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKNQFNDYTSKESCV 600
DB 541 KLRAPQCRPMTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKNQFNDYTSKESCV 600
QY 601 GL 602
DB 601 GL 602

RESULT 2
Q9NIN9 PRELIMINARY; PRT; 602 AA.
AC Q9NIN9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Butyrylcholinesterase (EC 3.1.1.8).
GN Name=BChE;
OS Equus caballus (Horse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20181263; PubMed=10718335;
RA Mierdl M., Morton C.L., Danks M.K., Potter P.M.;
RT "Isolation and characterization of a cDNA encoding a horse liver
RT butyrylcholinesterase: evidence for CPT-11 drug activation.";
RL Biochem. Pharmacol. 55:773-781(2000).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF178685; AAF61480.1; -.
DR HSP; P21836; INSM.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000979; Cholinesterase.
DR InterPro; IPR000379; Ser. esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 602 AA; 68838 MW; 94C73F00431DF26E CRC64;

Query Match 87.7%; Score 2858; DB 2; Length 602;
Best Local Similarity 89.6%; Pred. No. 1.6e-206;
Matches 537; Conservative 20; Mismatches 42; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKRGVGNLTVPFGTVAFLGIP 60
DB 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKRGVGNLTVPFGTVAFLGIP 60
QY 61 YAOPLGRRLRFFKKRQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120
DB 61 YAOPLGRRLRFFKKRQSLTKMSDIWNAATKYANSCCONIDQSPFGHSGEMNPNPTDLSDC 120
QY 121 LYINWVLPAPKPKNAATVLMVYGGGQOTGSSLVYDGKFLARVERIYVSMYRVGALG 180
DB 121 LYINWVLPAPKPKNAATVLMVYGGGQOTGSSLVYDGKFLARVERIYVSMYRVGALG 180
QY 181 FLALPGNPEAPGNMGLFDQDLALOWVOKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
DB 181 FLALPGNPEAPGNMGLFDQDLALOWVOKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
QY 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKDPQEI 300
DB 241 SHSLFTRAILIQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKDPQEI 300
QY 301 LLINEAFVYVPGTPLSVNFGPTVDGLTMDPDLLELQPKTKQIILGVNKKDEBTAAVY 360
DB 301 LLINEAFVYVPGTPLSVNFGPTVDGLTMDPDLLELQPKTKQIILGVNKKDEBTAAVY 360
QY 361 GAGPFSKDNNSITTRKFEQGLKIFPGVSEFGKESILFHYTPWVDORPENYREALGDV 420
DB 361 GAGPFSKDNNSITTRKFEQGLKIFPGVSEFGKESILFHYTPWVDORPENYREALGDV 420
QY 421 VGDYNPICPALPFTKSEWGNNAFFYYFEHRSSKLPWPMWGMGVEIEFVFGLEPLER 480
DB 421 VGDYNPICPALPFTKSEWGNNAFFYYFEHRSSKLPWPMWGMGVEIEFVFGLEPLER 480

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QY 301 LLINEAVPVPYGTPLSVNFGPTVDGDELTPMDPILLEGPKTKQILVGNKDEGTWFLVY 360
 DB 301 LLINEAVPVPYGTPLSVNFGPTVDGDELTPMDPILLEGPKTKQILVGNKDEGTWFLVY 360
 QY 361 GARPFSKDNNSIITRKEFGGLKI FPPGVSEFGKESILFHYTWDVDORPENYREALGVY 420
 DB 361 GARPFSKDNNSIITRKEFGGLKI FPPGVSEFGKESILFHYTWDVDORPENYREALGVY 420
 QY 421 VGDNVFCPLAEFKKSEWGNNAFFYYFHRSSKLPWPMGMGMGYZIEFVGLPLER 480
 DB 421 VGDNVFCPLAEFKKSEWGNNAFFYYFHRSSKLPWPMGMGMGYZIEFVGLPLER 480
 QY 481 RDNTYKAEILSRISVIRKMANFAKYGNPNSTONNSISWVPFKSTEQKYLTLNSTRINT 540
 DB 481 RDNTYKAEILSRISVIRKMANFAKYGNPNSTONNSISWVPFKSTEQKYLTLNSTRINT 540
 QY 541 KLRAGQCRFWTSPFKYLEMTGNTIDEAEWEKAGFHRNNYMDMKQFNDYTSKES 599
 DB 541 KLRAGQCRFWTSPFKYLEMTGNTIDEAEWEKAGFHRNNYMDMKQFNDYTSKES 599
 RESULT 3
 CHLE_RABIT STANDARD; PRT; 581 AA.
 ID CHLE_RABIT STANDARD; PRT; 581 AA.
 AC P21927;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (acetylcholine acylhydrolase)
 DE (Choline esterase II) (butyrylcholine esterase)
 DE (Pseudochoolinesterase).
 DE Name=BCHE;
 OS Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RX STRAIN=New Zealand;
 RX MEDLINE=90326526; PubMed=2374720;
 RA "Jbilo O., Roudani S., Chatonnet A.;
 RT "Complete sequence of rabbit butyrylcholinesterase.";
 RL Nucleic Acids Res. 18:3990-3990(1990).
 RN [2]
 RP SEQUENCE FROM 75-215 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91201348; PubMed=2016308;
 RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
 RA Barthele C.F., Nogueira C.P., la Du B.N., Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 RT butyrylcholinesterase from several vertebrates.";
 RL J. Biol. Chem. 266:6966-6974(1991).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
 CC two subunits in a dimer are linked by a disulfide bond.
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
 CC organophosphorus esters.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X52090; CAA36308.1; -
 CC DR EMBL; X52091; CAA36308.1; JOINED.
 CC DR EMBL; X52092; CAA36308.1; JOINED.

DR EMBL; M62779; AAA31169.1; -
 DR PIR; S10255; C39768.
 DR HSSP; P2303; 1P8U. Carbesteraeb.
 DR InterPro; IPR002018; Cholinesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser-estrs.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00678; CHOLINESTRAS.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Glycopoltein; Hydrolase; Serine esterase; Signal.
 FT SIGNAL 1 581
 FT CHAIN 9
 FT ACT SITE 205 205
 FT ACT SITE 332 332
 FT ACT SITE 445 445
 FT DISULFID 72 99
 FT DISULFID 259 270
 FT DISULFID 407 526
 FT DISULFID 578 578
 FT CARBOHYD 113 113
 FT CARBOHYD 248 248
 FT CARBOHYD 263 263
 FT CARBOHYD 348 348
 FT CARBOHYD 462 462
 FT CARBOHYD 488 488
 FT CARBOHYD 492 492
 FT CARBOHYD 493 493
 SQ SEQUENCE 581 AA; 66156 MW; F8B1997B32EB0A CMC64;
 Query Match 87.6%; Score 2855.5; DB 1; Length 581;
 Best local similarity 91.4%; Pred. No. 2.3e-206;
 Matches 531; Conservative 12; Mismatches 37; Indels 1; Gaps 1;
 QY 21 MLIGKSHEDDIIITAKNKVKGMLTVFGGVTAFLGIPYAOPLGRPKKPSQILKW 80
 DB 1 MYRRSHTE-DVITTKNKRIRGINLPVFGGVTAFLGIPYAOPLGRPKKPSQILKW 59
 QY 81 SDIWNATKYANCCQNIIDSPFGFSGEMWMENTDLSBDCLYNWIPAPKPKATVLIW 140
 DB 60 SDIWNATKYANCCQNIIDSPFGFSGEMWMENTDLSBDCLYNWIPAPKPKATVLIW 119
 QY 141 IYGGGFQGTSSILAVYDGFKLARVERIVYVSNVYVAGLFGALNGNEAPGMGLPDQ 200
 DB 120 IYGGGFQGTSSILAVYDGFKLARVERIVYVSNVYVAGLFGALNGNEAPGMGLPDQ 179
 QY 201 LALOWOKNIAAFAGNPKSVTLFGESAGASVLSHLSPGSHLFTRAILOGSSFNAPWA 260
 DB 180 LALOWOKNIAAFAGNPKSVTLFGESAGASVLSHLSPGSHLFTRAILOGSSFNAPWA 239
 QY 261 VTSIYKARNETLNAKLTGCSRNETEITIKLRNKPQELINEAVVYVYGPPLVNGP 320
 DB 240 VMSIHEARNETLNAKLTGCSRNETEITIKLRNKPQELINEAVVYVYGPPLVNGP 299
 QY 321 TVDGDPLTMDPDLLELGQKTKQILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOE 380
 DB 300 TVDGDPLTMDPDLLELGQKTKQILVGNKDEGTWFLVYAGPFSKDNNSIITRKEFOE 359
 QY 381 GLKIFPFGVSEFGKESILFHYTWDVDORPENYREALGVYDYNFCPLAEFTKFS 440
 DB 360 GLKIFPFGVSEFGKESILFHYTWDVDORPENYREALGVYDYNFCPLAEFTKFS 419
 QY 441 GNNAFYYFHRSSKLPWPMGMGMGYZIEFVGLPLERDNTYKAEILSRISVIRKMA 500
 DB 420 GNNAFYYFHRSSKLPWPMGMGMGYZIEFVGLPLERDNTYKAEILSRISVIRKMA 479
 QY 501 NFATYGNPNSTONNSISWVPFKSTEQKYLTLNSTRINTKLRAGQCRFWTSPFKYLEM 560
 DB 480 NFATYGNPNSTONNSISWVPFKSTEQKYLTLNSTRINTKLRAGQCRFWTSPFKYLEM 539
 QY 561 TGNIDEAEWEKAGFHRNNYMDMKQFNDYTSKESCVG 601

DB 540 TGNIDEAEQEMKAGFHRMNNYMMAMKHFNDYTSKERCAG 560

RESULT 4
CHIE_FELCA STANDARD; PRT; 602 AA.
AC 062760;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCH;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.
OK NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Plutary;
RX MEDLINE=20334351; PubMed=10874122;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma."
RL Biochem. Pharmacol. 60:479-487(2000).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond (By
CC similarity).
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters (By similarity).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC EMBL: AF053483; AAC06261.1; -.
DR HSP, P22303; 1B41.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser esters.
DR Pfam: PF00135; Coesterase.1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 602 Cholinesterase.
FT ACT_SITE 226 226 Acyl-ester intermediate (By similarity).
FT ACT_SITE 353 353 Charge relay system (By similarity).
FT ACT_SITE 466 466 Charge relay system (By similarity).
FT DISULFID 93 120 By similarity.
FT DISULFID 280 291 By similarity.
FT DISULFID 428 547 By similarity.
FT DISULFID 599 599 Interchain (By similarity).
FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 269 269 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 483 483 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).

SEQ SEQUENCE 602 AA; 68328 MW; ECB8879232B74B9C CRC64;

Query Match 85.4%; Score 2784; DB 1; Length 602;
Best Local Similarity 86.9%; Pred. No. 6e-201;
Matches 523; Conservative 24; Mismatches 55; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRPLFWLLCMLIGKSHTEDDIIATKNGKVRGNTLVFGYTAFFGIP 60
DB 1 MOSKGTIISQIFLRFLLVLLIGKSHTEDDIIITKNGKVRGNTLVFGYTAFFGIP 60
QY 61 YAPPLGRLEPKFPOSITKMSDIWNATKYANSCCONIDSPFPHSEMNPMTDISED 120
DB 61 YAPPLGRLEPKFPOSITKMSDIWNATKYANSCYQNAQSPFPOSSEMNPMTDISED 120
QY 121 LYANVWIPAKPKNAATVLIWYGCFOTGSSLHVDGKELAVERYIVVSMYRVGALG 180
DB 121 LYANVWIPAKPKNAATVLIWYGCFOTGSSLHVDGKELAVERYIVVSMYRVGALG 180
QY 181 FLALPGNPEAPGNGLPDQQLALQWYQKNIATFGNPKSVTLFGESAGAAVSLLHLSPG 240
DB 181 FLALPGNPEAPGNGLPDQQLALQWYQKNIATFGNPKSVTLFGESAGAAVSLLHLSPG 240
QY 241 SHSLFTRATIGSSFPAPAAVTSIYERARNTLALATGSRNENETIKCLNNKPOEI 300
DB 241 SQPLFTRATIGSSSNAPAAVTSIYERARNTLALATGSRNENETIKCLNNKPOEI 300
QY 301 LLINEAFVPGYPTPLSVNFGPTVDGDFLTMDPDLLEIGQPKTQILVGVKDEGTWFLV 360
DB 301 LLINEAFVPGYPTPLSVNFGVVDGDFLTMDPDLLEIGQPKTQILVGVKDEGTWFLV 360
QY 361 GAFGFSKDNNSITTRKFOGKIIFPPGVSEFKESILFHYTWDVDDQRPENTREALGV 420
DB 361 GAFGFSKDNNSITTRKFOGKIIFPPGVSEFKESILFHYTWDVDDQRPENTREALGV 420
QY 421 VGVNFIICPLLETFTKFSSEWGNNAFFYFPHRSKLPMPWPMVMGYLEIFPGPLER 480
DB 421 VGVNFIICPLLETFTKFSSEWGNNAFFYFPHRSKLPMPWPMVMGYLEIFPGPLER 480
QY 481 RDVYTKAEILISIVKMANFAKYGPNETQNNSTWPFKSTEQKYLTLNTESTRIMT 540
DB 481 RVYTKAEILISIVKMANFAKYGPNETQNNSTWPFKSTEQKYLTLNTESTRIMT 540
QY 541 KLRAGQCRFTSFPKVLWMTGNIDEAEWEMKAGFHRMNNYMMAMKHFNDYTSKESCA 600
DB 541 KLRAGQCRFTSFPKVLWMTGNIDEAEWEMKAGFHRMNNYMMAMKHFNDYTSKESCA 600
QY 601 GL 602
DB 601 GL 602
QY 601 GL 602
DB 601 GL 602

RESULT 5
CHIE_HORSE STANDARD; PRT; 574 AA.
AC P81908;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (Eq-
DE BCHB).
GN Name=BCH;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OK NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA Moorad D.R., Luo C., Garcia G.B., Doctor B.P.;
RT "Amino acid sequence of horse serum butyrylcholinesterase."
RL (in) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.
(eds.);

RL Structure and function of cholinesterases and related proteins,
 RL pp.145-146, Plenum Press, New York and London (1998).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
 CC two subunits in a dimer are linked by a disulfide bond.
 CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
 CC organophosphate esters.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC HSSP; P21836; INSM.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser. esters.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Direct protein sequencing: Glycoprotein; Hydrolyase; Serine esterase.
 FT ACT_SITE 198 198 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 325 325 Charge relay system (By similarity).
 FT ACT_SITE 438 438 Charge relay system (By similarity).
 FT ACT_SITE 65 92 By similarity.
 FT DISULFID 252 263 By similarity.
 FT DISULFID 400 519 By similarity.
 FT DISULFID 571 571 Interchain (By similarity).
 FT CARBOHYD 57 57 N-linked (GlcNAc. . .).
 FT CARBOHYD 106 106 N-linked (GlcNAc. . .).
 FT CARBOHYD 241 241 N-linked (GlcNAc. . .).
 FT CARBOHYD 256 256 N-linked (GlcNAc. . .).
 FT CARBOHYD 341 341 N-linked (GlcNAc. . .).
 FT CARBOHYD 455 455 N-linked (GlcNAc. . .).
 FT CARBOHYD 481 481 N-linked (GlcNAc. . .).
 FT CARBOHYD 486 486 N-linked (GlcNAc. . .).
 SQ SEQUENCE 574 AA; 65641 MW; 07755E9F9CB3E CRC64;
 Query Match 85.1%; Score 2774; DB 1; Length 574;
 Best Local Similarity 90.5%; Pred. No. 3,2e-200;
 Matches 517; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

DB 481 NETONNSRTRMFWFKSTBOKYLTLNTESTRIWTKLRAQCCRFWTSFPPVLEMTGNIDBAE 540
 QY 569 WEKAGFHRNNYMMDNKNQPDYTSKKEC 599
 DB 541 REMKAGFHRNNYMMDNKNQPDYTSKKEC 571
 RESULT 6
 CHIE_PANTT
 ID CHIE_PANTT STANDARD, PRT; 602 AA.
 AC 062761;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (pseudocholinesterase).
 GN Name=BCH;
 OS Panthera tigris tigris (Bengal tiger).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
 OX NCBI_TaxID=7435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Plutary;
 RX MEDLINE=20334351; PubMed=10874122;
 RA Bartels C.P., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
 RA Lockridge O.;
 RT "Determination of the DNA sequences of acetylcholinesterase and
 RT butyrylcholinesterase from cat and demonstration of the existence of
 RT both in cat plasma."
 RL Biochem. Pharmacol. 60:479-487(2000).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
 CC two subunits in a dimer are linked by a disulfide bond (By
 CC similarity).
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
 CC organophosphate esters (By similarity).
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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 CC EMBL; AF053484; AAC06262.1; -.
 DR HSSP; P22303; 1B41.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser. esters.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Glycoprotein; Hydrolyase; Serine esterase; signal.
 KW SIGNAL 1 28
 FT CHAIN 29 602
 FT ACT_SITE 226 226 Cholinesterase.
 FT ACT_SITE 353 353 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 466 466 Charge relay system (By similarity).
 FT ACT_SITE 93 120 Charge relay system (By similarity).
 FT DISULFID 280 291 By similarity.
 FT DISULFID 428 547 By similarity.
 FT DISULFID 599 599 Interchain (By similarity).
 FT CARBOHYD 85 85 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 134 134 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 269 269 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 284 284 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 369 369 N-linked (G1cNac. . .) (Potential).
 FT CARBOHYD 483 483 N-linked (G1cNac. . .) (Potential).
 FT CARBOHYD 509 509 N-linked (G1cNac. . .) (Potential).
 FT CARBOHYD 513 513 N-linked (G1cNac. . .) (Potential).
 FT CARBOHYD 514 514 N-linked (G1cNac. . .) (Potential).
 SQ SEQUENCE 602 AA; 68289 MW; EB0CB9148B956A1 CRC64;
 Query Match 85.0%; Score 2772; DB 1; Length 602;
 Best Local Similarity 86.5%; Pred. No. 4,8e-200;
 Matches 521; Conservative 25; Mismatches 56; Indels 0; Gaps 0;
 QY 1 MDKAVTITICRFLFWLLCMLIKSHTEDDIIATNGKRGKMLTVFGSTVAFGIP 60
 DB 1 MOSKGTIISIQFLIRFLMLWLIKSHTEBDIIITTKGKRGKMLPLDGTVAFAFGIP 60
 QY 61 YAOPLRLRPKPKQFLTKSDINATKYNASCONIDQSPFGHSEMMNPNTDLSBDC 120
 DB 61 YAOPLRLRLRPKPKQFLTKSDINATKYNASCONIDQSPFGHSEMMNPNTDLSBDC 120
 QY 121 LYLVNWIIPAKPKNATVLIWYGGGFGTGTSSLHVYDGKFLARVERIVVSMYRVGALG 180
 DB 121 LYLVNWIIPAKPKNATVLIWYGGGFGTGTSSLHVYDGKFLARVERIVVSMYRVGALG 180
 QY 181 FLALPGNPEAPGNNGLPDQALQWQKNTAFAFGNPKSVTLFGESAGASVSLHLSPG 240
 DB 181 FLALPGNPEAPGNNGLPDQALQWQKNTAFAFGNPKSVTLFGESAGASVSLHLSPR 240
 QY 241 SHSLFTTALIQSGSFNAPVATSLYEARNRTLAKLTGCRNEMETIKLARKDPOEI 300
 DB 241 SHSLFTTALIQSGSFNAPVATSLYEARNRTLAKLTGCRNEMETIKLARKDPOEI 300
 QY 301 LNEAFVVPYGTPTSVNPGFTVDDPFLTMDPDLLEFGPKTKIIVGVNDEGTWFLVY 360
 DB 301 LNEAFVVPYGTPTSVNPGFTVDDPFLTMDPDLLEFGPKTKIIVGVNDEGTWFLVY 360
 QY 361 GAPFSKDNNSIITRKESFQEGKIFPGVSEFGKESILFHTYDWDQDPENYREALGDV 420
 DB 361 GAPFSKDNNSIITRKESFQEGKIFPGVSEFGKESILFHTYDWDQDPENYREALDV 420
 QY 421 VGDVNFICPALFETKSEMNNAFFYFHEHRSKLTWPEMGMGMEYIEFVGLFLER 480
 DB 421 VGDVNFICPALFETKSEMNNAFFYFHEHRSKLTWPEMGMGMEYIEFVGLFLER 480
 QY 481 RDNYTKAEILSRISIVKMANFAKYNPNETONNSTMPVKESTEOXYLTINTESTRIMT 540
 DB 481 RDNYTKAEILSRISIVKMANFAKYNPNETONNSTMPVKESTEOXYLTINTESTRIMT 540
 QY 541 KLRAGQCRFWTSPFKYLEMTGNIDAEWEKAGFHRMNNYMDWKQOFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSPFKYLEMTGNIDAEWEKAGFHRMNNYMDWKQOFNDYTSKESCA 600
 QY 601 GL 602
 DB 601 GL 602
 RESULT 7
 BAC34196 PRELIMINARY; PRT; 603 AA.
 AC BAC34196;
 DT 14-APR-2004 (Tremblrel. 27, Created)
 DT 14-APR-2004 (Tremblrel. 27, Last sequence update)
 DE 14-APR-2004 (Tremblrel. 27, Last annotation update)
 DE Adult male liver tumor cDNA, RIKEN full-length enriched library,
 DE clone: C730038G20 product: Ductylcholesterase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=1246851;

RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99279253; PubMed=1034636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20493374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sakaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwaiki K.,
 RA Fujikake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hamaguchi T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK050337; BAC34196.1;
 SQ SEQUENCE 603 AA; 68462 MW; 2CB79C46797B3713 CRC64;
 Query Match 79.8%; Score 2602; DB 2; Length 603;
 Best Local Similarity 80.5%; Pred. No. 3.1e-187;
 Matches 476; Conservative 47; Mismatches 68; Indels 0; Gaps 0;
 QY 12 FLFWLLCMLIKSHTEDDIIATNGKRGKMLTVFGSTVAFGIPYAOPLRLRP 71
 DB 13 FLFWLLCMLIKSHTEDDIIATNGKRGKMLTVFGSTVAFGIPYAOPLRLRP 72
 QY 72 KKPOSLTKMSDINATKYNASCONIDQSPFGHSEMMNPNTDLSBDCLYLVNWIIPAK 131
 DB 73 KKPOSLTKMSDINATKYNASCONIDQSPFGHSEMMNPNTDLSBDCLYLVNWIIPAK 132
 QY 132 PKNATVLIWYGGGFGTGTSSLHVYDGKFLARVERIVVSMYRVGALGPLAPNPEAP 191


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Db      133 PKNATVWVWYGGFGTSSLPVYDGKFLARVERIVVSMYRYGALGFLAPGNPDAP 192
Qy      192 GNNGLFPQOALQWQKNIAAFGNGPKSVTLPGESGAASVSLHLLSPGSHLFTRAIQ 251
Db      193 GNNGLFPQOALQWQKNIAAFGNGPKSVTLPGESGAASVSLHLLCPQSYLFTRAIQ 252
Qy      252 SSGSNAPWATSLYEARNRTLNIAKTGCSRENETIICKLRNKDQOELLNEAFVPG 311
Db      253 SSGSNAPWATSLYEARNRTLNIAKTGCSRENEMEMIKLRNKDQOELLNEAFVPG 312
Qy      312 TPLSVNGPVDGDFLTDMPDILLETGQPKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 371
Db      313 SILSINFGPYVDGDFLTDMPDILLETGQPKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 372
Qy      372 IITKEFQEGIKTFPPGVSEFGKESILFHYTDWVDQRPENRYEALGDVVDGYNFICPAL 431
Db      373 LITKEFQEGIKTFPPGVSEFGKESILFHYTDWVDQRPENRYEALGDVVDGYNFICPAL 432
Qy      432 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLGRVNTTRAELIF 491
Db      433 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLGRVNTTRAELIF 492
Qy      492 SRSIYKRWANPAKYGNETONSTSPVFEKTEOKLTLNTESTRIMTKLPAQOCRFMT 551
Db      493 SRSIYKRWANPAKYGNETONSTSPVFEKTEOKLTLNTESTRIMTKLPAQOCRFMT 552
Qy      552 SFPFKVLEMTGNIDEAEMWKAFFHNNVMMWKNQFNQDYSKESCVGL 602
Db      553 LFPFKVLEMTGNIDEAEMWKAFFHNNVMMWKNQFNQDYSKESCVGL 603

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RESULT 8

CHLE MOUSE STANDARD; PRT; 603 AA.

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AC 00311:
ID CHLE MOUSE STANDARD; PRT; 603 AA.
AC 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudochoolinesterase).
CN Name:Boche;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90380429; PubMed=240605;
RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT of alternatively spliced mRNA species."
RL Neuron 5:317-327(1990).
RN [2]
RP SEQUENCE OF 97-237 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Appaous M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Barthele C.F., Nogueira C.B., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates."
RL J. Biol. Chem. 266:6966-6974(1991).
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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DR EMBL: M99492; AAA37328.1;
DR PIR: S70849; S70849.
DR HSSP: P22303; 198U.
DR MGD: MGI:894278; Bcne.
DR InterPro: IPR002018; Carbesterease.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR003379; Ser ester.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYL-ESTERASE B.1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE B.2; 1.
DR GlycoProtein: Hydrolyase; Serine esterase; Signal.
KW SIGNAL
FT CHAIN 1 29
FT ACT_SITE 30 603 Cholinesterase.
FT ACT_SITE 227 227 Acyl-ester intermediate (By similarity).
FT ACT_SITE 354 354 Charge relay system (By similarity).
FT ACT_SITE 467 467 Charge relay system (By similarity).
FT DISULFID 94 121 By similarity.
FT DISULFID 281 292 By similarity.
FT DISULFID 429 548 By similarity.
FT DISULFID 600 600 Interchain (By similarity).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (potential).
FT CARBOHYD 270 370 N-linked (GlcNAc...) (potential).
FT CARBOHYD 370 370 N-linked (GlcNAc...) (potential).
FT CARBOHYD 484 484 N-linked (GlcNAc...) (potential).
FT CARBOHYD 510 510 N-linked (GlcNAc...) (potential).
FT CARBOHYD 515 515 N-linked (GlcNAc...) (potential).
FT CONFLICT 129 129 R -> P (in Ref. 2).
SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;

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Query Match 79.5%; Score 2593; DB 1; Length 603;
Best Local Similarity 80.4%; Pred. No. 1,5e-186;
Matches 475; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

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Qy 12 FLFWPLLCMLIGKSTEDDIIATKNGKVRGMNLTVGTVTAFLGIPYQPLGRURF 71
Db 13 FLFWPLLCMLIGKSTEDDIIATKNGKVRGMNLTVGTVTAFLGIPYQPLGRURF 72
Qy 72 KKPQSLTKNSDIWNAATKYNANSCCNIDQSPFGHSEKMNPTDISEDCLYANWIRPK 131
Db 73 KKPQSLTKNSDIWNAATKYNANSCCNIDQSPFGHSEKMNPTDISEDCLYANWIRPK 132
Qy 132 PKNATVWVWYGGFGTSSLPVYDGKFLARVERIVVSMYRYGALGFLAPGNPDAP 191
Db 133 PKNATVWVWYGGFGTSSLPVYDGKFLARVERIVVSMYRYGALGFLAPGNPDAP 192
Qy 192 GNNGLFPQOALQWQKNIAAFGNGPKSVTLPGESGAASVSLHLLSPGSHLFTRAIQ 251
Db 193 GNNGLFPQOALQWQKNIAAFGNGPKSVTLPGESGAASVSLHLLCPQSYLFTRAIQ 252
Qy 252 SSGSNAPWATSLYEARNRTLNIAKTGCSRENETIICKLRNKDQOELLNEAFVPG 311
Db 253 SSGSNAPWATSLYEARNRTLNIAKTGCSRENEMEMIKLRNKDQOELLNEAFVPG 312
Qy 312 TPLSVNGPVDGDFLTDMPDILLETGQPKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 371
Db 313 SILSINFGPYVDGDFLTDMPDILLETGQPKKTQILVGVNDEGTWFLVYGAPEFSKDNDS 372
Qy 372 IITKEFQEGIKTFPPGVSEFGKESILFHYTDWVDQRPENRYEALGDVVDGYNFICPAL 431
Db 373 LITKEFQEGIKTFPPGVSEFGKESILFHYTDWVDQRPENRYEALGDVVDGYNFICPAL 432
Qy 432 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLGRVNTTRAELIF 491
Db 433 EFTKKFSEMGNNAPFFYFEHRSKLPWEMWGVHGEIEFVGLPLGRVNTTRAELIF 492

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QY 492 SRSIVKMANFAXYGNPNETONNSTWPFVFKSTBOXYLTLLTTESTRITMTKLRACQCRFMT 551
 DB 493 SRSIMKTWANFAXYGNPNETONNSTWPFVFKSTBOXYLTLLTTESTRITMTKLRACQCRFMT 552
 QY 552 SFPKPVLEMTGNIDEAEWEMKAGFHRNNNNYMDKNOFNNDYTSKESCGVL 602
 DB 553 LFPKPVLEMTGNIDEAEWEMKAGFHRNNNNYMDKNOFNNDYTSKESCGVL 603

RESULT 9

090KCI PRELIMINARY; PRT; 597 AA.
 ID 090KCI
 AC 090KCI; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DB Butyrylcholinesterase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Liu A.M., Lockridge O., Bartels C.F.;
 RA BrimJoin S., Hinrichs S.H., Lockridge O.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AF244349; AAF44713.1; -.
 DR HSP; P22303; 1F8U.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004104; F:cholinesterase activity; IEA.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLNSTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7EBAC CRC64;

Query Match 79.4%; Score 2588; DB 2; Length 597;
 Best Local Similarity 79.8%; Pred. No. 3.5e-186;
 Matches 473; Conservative 47; Mismatches 73; Indels 0; Gaps 0;

QY 10 IRPLFWLLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGYTAFLGIPYAOPLGRL 69
 DB 5 IHFLMLTLLCMLFGKSHTEDEVIITTKTGRVGRSLSPHIIAGITVAFGIPYAOPLGSL 64
 QY 70 RPKKPOSLLTKMSDINATKYNANSCONIDOSFPGFHSSEMMNPNTDISEDCLYINWIPA 129
 DB 65 RPKKPOSLLTKMSDINATKYNANSCONIDOSFPGFHSSEMMNPNTDISEDCLYINWIPA 124
 QY 130 PKPKNATVLWYGGGFQGTSSLAHVVDGKFLAVERIVVSNMYRVGALGFLALPGNPE 189
 DB 125 PKPKNATVLWYGGGFQGTSSLAHVVDGKFLAVERIVVSNMYRVGALGFLALPGNPE 184
 QY 190 APGNGMFLPDQOLALQWQKNTAAFGNPKSYTLFGEAGAAVSLLHLSPGSHLFTFRAI 249
 DB 185 APGNGMFLPDQOLALQWQKNTAAFGNPKSYTLFGEAGAAVSLLHLSPGSHLFTFRAI 244
 QY 250 LOSGSPAPNAVATSLYEARNRTLLAKLTLGCSRENETEIIKCLANKPOEILLNEAFVFP 309
 DB 245 LBSGSSNAFNAVATSLYEARNRTLLAKLTLGCSRENETEIIKCLANKPOEILLNEAFVFP 304
 QY 310 YGTPLSVNFPGTYVDGFLTDMPIILBLQGFKKTQIILGVNKGEGTWFLVYGAFGFSKDN 369

DB 305 SDSIRSINFPRTYDVGFLTDMPTLLQLGKVAQIILGVNKGEGTWFLVYGAFGFSKDN 364
 QY 370 NSIITRKEPOGLKIFPGVSEFGKESILFHYTDWDDORPENYREALGVNGLYNICP 429
 DB 365 DSLITRKEPOGLKIFPGVSEFGKESILFHYTDWDDORPENYREALGVNGLYNICP 424
 QY 430 ALBETKFSSEWGNNAFPYYPBHRSSKLPWPEWGVNHYEIEFVGLPLERRDNYTAEB 489
 DB 425 ALBETKFSSEWGNNAFPYYPBHRSSKLPWPEWGVNHYEIEFVGLPLERRDNYTAEB 484
 QY 490 ILRSIVKMANFAXYGNPNETONNSTWPFVFKSTBOXYLTLLTTESTRITMTKLRACQCRF 549
 DB 485 ILRSIVKMANFAXYGNPNETONNSTWPFVFKSTBOXYLTLLTTESTRITMTKLRACQCRF 544
 QY 550 WTSFPPVLEMTGNIDEAEWEMKAGFHRNNNNYMDKNOFNNDYTSKESCGVL 602
 DB 545 WTSFPPVLEMTGNIDEAEWEMKAGFHRNNNNYMDKNOFNNDYTSKESCGVL 603

RESULT 10

090ZK8 PRELIMINARY; PRT; 603 AA.
 ID 090ZK8
 AC 090ZK8; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DB Butyrylcholinesterase precursor (EC 3.1.1.8).
 GN Name-BCH;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Geisler K., Chatonnet A., Layer P.G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AJ306328; CAC37792.1; -.
 DR HSP; P21836; 1NSM.
 DR GO; GO:0004104; F:cholinesterase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLNSTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Signal.
 FT SIGNAL 1
 FT CHAIN 30 603 butyrylcholinesterase.
 SQ SEQUENCE 603 AA; 68480 MW; A350FDD68574ADF CRC64;

Query Match 71.8%; Score 2339.5; DB 2; Length 603;
 Best Local Similarity 71.9%; Pred. No. 1.9e-167;
 Matches 427; Conservative 70; Mismatches 96; Indels 1; Gaps 1;

QY 8 ICIRFLFWLLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGYTAFLGIPYAOPLG 67
 DB 9 ICARFLMWLLLCMLFGRKRVPEEDN-VITTEKGRVGRGNLQVLGIVTAFGIPYKRPBG 67
 QY 68 RLPKPOSLLTKMSDINATKYNANSCONIDOSFPGFHSSEMMNPNTDISEDCLYINWIPA 127
 DB 68 RLPKPOSLLTKMSDINATKYNANSCONIDOSFPGFHSSEMMNPNTDISEDCLYINWIPA 127
 QY 128 PAKPKNATVLWYGGGFQGTSSLAHVVDGKFLAVERIVVSNMYRVGALGFLALPGN 187
 DB 128 PAKPKNATVLWYGGGFQGTSSLAHVVDGKFLAVERIVVSNMYRVGALGFLALPGN 187
 QY 188 PAKPKNATVLWYGGGFQGTSSLAHVVDGKFLAVERIVVSNMYRVGALGFLALPGN 247
 DB 188 PAKPKNATVLWYGGGFQGTSSLAHVVDGKFLAVERIVVSNMYRVGALGFLALPGN 247

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Db 188 KEVPGNAGLFDQRLALQWQENTASRGQNKSVTTIGESAGASVSYHILSPKSHPLFR 247
Qy 248 AILQSGSFNPMWAVTSIYEARNRTLNLAKLTCGSRNEETELIKLNNKQPOBILNEAFV 307
Db 248 AILQSGSFNPMWAVTSIYEARNRTLNLAKLTCGSRNEETELIKLNNKQPOBILNEAFV 307
Qy 308 VPGTPLSVNPGFTVDGFLTMDPDLLELQGRKQIILVGNKDKDGMFLVYAGAPFK 367
Db 308 VKYFSLHIFCPVDVDFLADMEALIKNGIFKQIQLVGNKDKDGMFLVYAGAPFK 367
Qy 368 DNNGLITRKEPOBGLKIFPGVSEFGKESILFHYTDVDDQPRENRYREALGVVDYNTL 427
Db 368 DSDSLINKTQPEVALTISFPQVSKLAEISIIFYQTDWENQKXEHRRADMDVIGYHII 427
Qy 428 CPALFTKSGSEWNNAPFFYFEHRSKSLPMPKMGVMEGTEIFVVGFLERDNYTKA 487
Db 428 CPVAEFAKTLAEVGNANFFYFEHRSKSLPMPKMGVMEGTEIFVVGFLERDNYTKA 487
Qy 488 EELISRSIVKRNAPAKYGNPNQNNSTSPVKSTEOXYTLNTESTRIIMTKLRAQOC 547
Db 488 EELISRSIVKRNAPAKYGNPNQNNSTSPVKSTEOXYTLNTESTRIIMTKLRAQOC 547
Qy 548 RFTMFPFKVLEMTGNIDEAEMWKAQGFHRNNNTMMDKQFNDYTSKESCVG 601
Db 548 RFTMFPFKVLEMTGNIDEAEMWKAQGFHRNNNTMMDKQFNDYTSKESCVG 601

RESULT 11
ACES_ELEBL STANDARD; PRT; 633 AA.
ID ACES_ELEBL
AC 042275:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
OC Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN NCBI_TaxID=8005;
RP SEQUENCE FROM N.A.
RX MEDLINE=98070504; PubMed=9407087;
RA Simon S., Massoulié J.;
RT "Cloning and expression of acetylcholinesterase from Electrophorus.
RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
RT cells."
RL J. Biol. Chem. 272:33045-33055(1997).
CC - FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC - CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC - SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF030422; AAB8606.1; -.
CC DR HSSP; P04058; I123.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW Serine esterase; Signal; Synapse.
FT SIGNL 1 23 Potential.
FT CHAIN 24 633 Acetylcholinesterase.

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FT ACT_SITE 225 225 Acyl-ester intermediate (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT ACT_SITE 494 494 Charge relay system (By similarity).
FT DISULFID 91 118 By similarity.
FT DISULFID 279 290 By similarity.
FT DISULFID 427 579 By similarity.
FT DISULFID 630 630 Interchain (By similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;

Query Match 54.5%; Score 1777; DB 1; Length 633;
Best Local Similarity 52.4%; Pred. No. 4,8e-125;
Matches 328; Conservative 108; Mismatches 150; Indels 40; Gaps 7;

Qy 12 FLFWFLLCMLIGKSHTEDDIIATKNGKVRGMILTVFGGT-VTAFGLIPYAPPLGRIR 70
Db 13 FLWFPLHLISI---AQTPDELLIMTRLGQVQGTBLPVDRSHVIAFLGIPRAEPLGMR 68
Qy 71 FKXPOSILTKSDINWATKANSCCNTDQSPRGHSGMNNPNTDLSBDCLYLVWVIPA- 129
Db 69 FKPEPKKPMNDVFPARYPKACYQVDTSTYSGESGTEMMKPNRMSBDCLYLVWVIPA- 128
Qy 130 PKPKNATVLIWITYGGAFQGTSSLHVYDGKFLARVERVIVVSMNVYAGALFLALPGNPE 189
Db 129 PKPHNLTWVWVITYGGAFYSGSSSLVYDGRVLAHEKVVVSMNVYAGALFLALPGNPE 188
Qy 190 APGNMGLFDQRLALQWQENTASRGQNKSVTLTPEESGAASVSHILSPKSHPLFR 249
Db 189 APGNVGLDQRLALQWQENTASRGQNKSVTLTPEESGAASVSHILSPKSHPLFR 248
Qy 250 LOSGSMNAPWATSLYEARNRTLNLAKLTCGSRNEETELIKLNNKQPOBILNEAFV 309
Db 249 LOSGVNGEMWRTVSPDEARRRAIKGLVGCPCDNDTDLICLRKQDQIDQMLVLP 308
Qy 310 YGTPLSVNFPGFTVDGFLTMDPDLLELQGRKQIILVGNKDKDGMFLVYAGAPFK 369
Db 309 FSGLFKFSFVPIVDGVPPDTEAMLNSGNFQDQIILGVNONESYFLIYAGAPFKSDN 368
Qy 370 NSIITTKRKEPOBGLKIFPGVSEFGKESILFHYTDVDDQPRENRYREALGVVDYNTL 429
Db 369 ESLITREDFLGQVKSVPFANETGLEAVILQYTDWEDNPIKRNBAAMDIVGDHNVCP 428
Qy 430 ALFTKKFSR-----MGN-----NAFFYFEHRSKSLPME 460
Db 429 LQHPAKRYAQSILQGTGTAGQNLGKNSGASNSGVSYLVMYDHRASNLVWPE 488
Qy 461 WGVMEGYEIEFVFGLPLERRDNTYAEELLSRSLYKRNANPAKGNPNETQNNST 517
Db 489 WGVYHGEYIEFVFGLPLEKRLNLYTLEERKLSRMMKRYANAPRGNPINVDGSDISR 548
Qy 518 -WPFVSTEOXYTLNTESTRIIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAEMWKAQGF 576
Db 549 RWPFPSTEOXYTLNTESTRIIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAEMWKAQGF 608
Qy 577 RNNVYMDMKNQFNDYTSKESCVGL 602
Db 609 RNSSYMMHMKNQPDHY-SKQERCTNL 633

RESULT 12
ACES_BRARE STANDARD; PRT; 634 AA.
ID ACES_BRARE
AC Q9DDE3:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
KW Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW Serine esterase; Signal; Synapse.
FT SIGNL 1 23 Potential.
FT CHAIN 24 633 Acetylcholinesterase.

```


MEDLINE=96244524; PubMed=8674549;
 RA Cousin X., Crennon C., Graesi J., Meilah K., Cornu G., Sallou B.,
 RA Bon S., Massoulié J., Bon C.;
 RT "Acetylcholinesterase from Bungarus venom: a monomeric species";
 RL FEBS Lett. 387:196-200(1996).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,
 CC including collagen-tailed forms.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=T;
 CC IsoId=Q92035-2; Sequence=Displayed;
 CC Name=S;
 CC IsoId=Q92035-1; Sequence=VSP_008215;
 CC -1- TISSUE SPECIFICITY: Liver and muscle contain both isoform T and
 CC isoform S. Venom gland predominantly contains isoform S.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@1sb-sib.ch).
 CC
 CC EMBL: U54591; AAC59905.1; -;
 CC EMBL: AF045238; AAC16420.1; -;
 CC EMBL: AF045238; AAC16421.1; -;
 CC HSP: P04058; 1H23.
 CC InterPro: IPR002018; Carboxylesterase.
 CC InterPro: IPR000997; Cholinesterase.
 CC InterPro: IPR000998; Fish_ache.
 CC InterPro: IPR000379; Ser_eatrs.
 CC Pfam: PF00135; Coesterase; 1.
 CC PRINTS: PR00878; CHOLINESTRASE.
 CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 CC DR Alternative splicing; Direct protein degradation; Glycoprotein;
 CC KW Hydrolyase; Membrane; Neurotransmitter degradation; Serine esterase;
 CC KW Signal; Synapse.
 CC
 CC FT SIGNAL 1 28
 CC FT CHAIN 29 606
 CC FT ACT_SITE 231 231
 CC FT ACT_SITE 358 358
 CC FT ACT_SITE 471 471
 CC FT DISULFID 98 125
 CC FT DISULFID 285 296
 CC FT DISULFID 433 552
 CC FT DISULFID 603 603
 CC FT CARBOHYD 289 289
 CC FT CARBOHYD 374 374
 CC FT CARBOHYD 484 484
 CC FT CARBOHYD 564 564
 CC FT VARSPLIC 567 606
 CC
 CC FT MUTAGEN 101 101
 CC FT MUTAGEN 316 316
 CC FT CONFLICT 268 268
 CC FT CONFLICT 350 350
 CC FT SEQUENCE 606 AA; 68074 MW; B95998A8EAOB5709 CRC64;
 CC
 CC Query Match 53.1%; Score 1730.5; DB 1; Length 606;
 CC Best Local Similarity 51.9%; Pred. No. 1.56-121;
 CC Matches 308; Conservative 114; Mismatches 160; Indels 11; Gaps 4;

QY 14 FMF-LILC-----MLIGKSHTEDDIIATKNGKRGMLTYEGGTATFLGIPYAQPL 66
 Db 15 WMLDGLLIPSCVAVLGRRA--GELKVSQTQTSVAGLSPLVDGVHSAFLGIPFAAPPL 71
 QY 67 GRLEFKKPSQSLTKMSDIDMNAKYANSQCCNIDSPQFHSSEMMNPVTLSECLYLNW 126
 Db 72 GRMFLRPEPKPQNHLDATSKYPACQVVDVDSPEQFQTEWMNPNRQMSDECLYLNW 131
 QY 127 IPAPKKNATVLTWYGGGFGQTGSSLTAVYDGKFLARVEVIVASNMRYGALGPLALP 186
 Db 132 VPSRPPKAPLVLTWYGGGFGSAASLDVYDGRFLTYTQVNLVLSYRGAGLGLP 191
 QY 187 NPEAPGNNGLEPDQALATWVQKNIAAFGKPKSVTLTGESAGAASVSLHLSGSHLFT 246
 Db 192 SPAPGNGLDQDLALQWLNQNNHPFGGNPRATVFGESAGAASVGMHLSTQSRFLQ 251
 QY 247 RALIGSGFNAPMAVTSLYEARNTLNAKLTGSGRENEEITKLANKPOEILNEAF 306
 Db 252 RALIGSGFNAPMAVTFPABSRGRLALGKQLGCHFNNDDELVSCLSKNPQELIDEWS 311
 QY 307 VVPYGTPLSNVAGPVPVGDDELTPMDLILLEGPKQTQIIVGVNKGDTFLVYGAEGFS 366
 Db 312 VLPYKSIIRFPFVPTDSDFPDTPBAMLSGKPKETQVLGVKDGSLYFLIGLPGFS 371
 QY 367 KNNNSIITRKEFOEGLKIFPGVSEFKESILFHYTWDDQRPENTREALGVYGYNF 426
 Db 372 KNEBLSIADPLDEGVMSVPHANDIATDAVLQTTQDDQDNKREKREALDDIVGHNV 431
 QY 427 ICPALEFTKSESGNNNAFFYFHRSSKLPMPEMGVMHGYELFPGVGLERDNYTK 486
 Db 432 ICPVQFANDYAKRSKYAVLFDRASNLMPMPGVPBGHYLEFVGLPLANSLVTP 491
 QY 487 AEEILSRSLVKRWANPFAKYGNFNETQNNSTSPVFKSTEQKYLTLNTESTRIMTKLRQ 546
 Db 492 QEKELSRMRKRYANFARIGNPTDPADSGAMPYTAQPOVQLNTPLATOPSLRAQI 551
 QY 547 CREFTSFPKRVLEMTGNIDEAEWKKAGFHRNNYTMMDMKQFNDYTSKXSC 599
 Db 552 CAFWNHFLPLNATVDITEARQWKLBFHLSAYMMWIKSQFDHY-NKQDC 603
 RESULT 14
 ACES_HUMAN STANDARD; PRT; 614 AA.
 ID ACES_HUMAN
 AC P22303; Q16169; Q9BXPF;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
 GN Name=ACHE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9108577; PubMed=2263619;
 RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnatt A., Neville L.,
 RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Litson Y.,
 RA Zakut H.;
 RT "Molecular cloning and construction of the coding region for human
 RT acetylcholinesterase reveals a G + C-rich attenuating structure";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
 RN [2]
 RP SEQUENCE OF 521-614 FROM N.A.
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5";
 RL Nucleic Acids Res. 29:1352-1365(2001).

RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
 RN MEDLINE=94131004; PubMed=22997725;
 RX Karpel R., Ben Azi-Aluya R., Sternfeld M., Ehrlich G., Ginsberg D.,
 RA Tarroni P., Clementi F., Zakut H., Soreq H.;
 RT "Expression of three alternative acetylcholinesterase messenger RNAs
 RN in human tumor cell lines of different tissue origins.";
 RL Exp. Cell Res. 210:268-277(1994).
 RN [4]
 RP PARTIAL SEQUENCE.
 RN TISSUE=Erythrocyte;
 RX MEDLINE=89232135; PubMed=2714437;
 RA Chhajiani V., Derr D., Earles B., Schnell E., August T.;
 RT "Purification and partial amino acid sequence analysis of human
 RN erythrocyte acetylcholinesterase.";
 RL FEBS Lett. 247:279-282(1989).
 RN [5]
 RP MUTAGENESIS OF CYS-611.
 RX MEDLINE=92084699; PubMed=1748670;
 RA Velan B., Grosfeld H., Kromann C., Leitner M., Gozes Y., Lazar A.,
 RA Flashner Y., Marcus D., Cohen S., Shafferman A.;
 RT "The effect of elimination of intersubunit disulfide bonds on the
 RN activity, assembly, and secretion of recombinant human
 RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
 RN mutant.";
 RL J. Biol. Chem. 266:23977-23984(1991).
 RN [6]
 RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
 RX MEDLINE=92388112; PubMed=1517212;
 RA Shafferman A., Kromann C., Flashner Y., Leitner M., Grosfeld H.,
 RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
 RT "Mutagenesis of human acetylcholinesterase. Identification of residues
 RN involved in catalytic activity and in polypeptide folding.";
 RL J. Biol. Chem. 267:17640-17648(1992).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 35-574.
 RX MEDLINE=98304745; PubMed=9640563;
 RA Felder C.B., Botli S.A., Lifson S., Silman I., Sussman J.L.;
 RT "External and internal electrostatic potentials of cholinesterase
 RN models.";
 RL J. Mol. Graph. Model. 15:318-327(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.
 RX MEDLINE=20508217; PubMed=11053835; DOI=10.1107/S0907444900010659;
 RA Kryger G., Harel M., Gilek K., Tokor L., Velan B., Lazar A.,
 RA Kromann C., Barak D., Ariel N., Shafferman A., Silman I.,
 RA Sussman J.L.;
 RT "Structures of recombinant native and E202Q mutant human
 RN acetylcholinesterase complexed with the snake-venom toxin fasciculin-
 RT II.";
 RL Acta Crystallogr. D 56:1385-1394(2000).
 RN [9]
 RP VARIANT BLOOD GROUP Yt(B) ASN-353.
 RX MEDLINE=93256075; PubMed=8488842;
 RA Bartels C.F., Zelinski T., Lockridge O.;
 RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
 RN accounts for Yt blood group polymorphism.";
 RL Am. J. Hum. Genet. 52:928-936(1993).
 RN [10]
 RP FUNCTION. Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: Homotrimer; composed of disulfide-linked homodimers.
 CC interacts with PRIMA1. The interaction with PRIMA1 is required to
 CC anchor it to the basal lamina of cells and organize into tetramers
 CC (by similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P22303-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P22303-2; Sequence=VSP_001457;
 CC -1- POLYMORPHISM: ACHB is responsible for the Yt blood group system.
 CC The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group

	CC	antigens is a ytlc variation in position 353; His-353 corresponds to Yt(e) and the rare variant with Asn-353 to Yt(b).
	CC	-1-SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
	CC	-1-DATABASE: NME=Blood group antigen mutation database;
	CC	NOTE=Yt blood group system;
	CC	MW="http://www.bioc.aecom.yu.edu/bgmur/Yt.htm".
	CC	-----
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	DR	EMBL, M55040, AAA68151.1, "-"
	DR	EMBL, AF312032, AAK21003.1, "-"
	DR	EMBL, S71129, AAC60618.1, "-"
	DR	PIR, A39256, A39256.
	DR	PDB, 1B4I, X-ray; A=36-574.
	DR	PDB, 1F8U, X-ray; A=32-614.
	DR	PDB, 2CLJ, Model; @=32-574.
	DR	SWISS-2DPAGE, P22303, HUMAN.
	DR	Genev; HGNC:108, ACHE.
	DR	MIM, 100740, "-"
	DR	MIM, 112100, "-"
	DR	GO, GO:0005605; C:bassal lamina; NAS.
	DR	GO, GO:0005576; C:extracellular; TAs.
	DR	GO, GO:0042166; F:acetylcholine binding; NAS.
	DR	GO, GO:0003990; F:acetylcholinesterase activity; IMP.
	DR	GO, GO:0001540; F:beta-amylloid binding; TAs.
	DR	GO, GO:0042803; F:protein homodimerization activity; NAS.
	DR	GO, GO:0001507; P:acetylcholine breakdown in synaptic cleft; NAS.
	DR	GO, GO:0042992; P:amyloid precursor protein metabolism; TAs.
	DR	GO, GO:0007153; P:cell adhesion; TAs.
	DR	GO, GO:0008283; P:cell proliferation; TAs.
	DR	GO, GO:0006260; P:DNA replication; TAs.
	DR	GO, GO:0007517; P:muscle development; TAs.
	DR	GO, GO:0050714; P:positive regulation of protein secretion; TAs.
	DR	GO, GO:0009611; P:response to wounding; TAs.
	DR	GO, GO:0007416; P:synaptogenesis; TAs.
	DR	InterPro, IPR002018, CarbesteraasB.
	DR	InterPro, IPR000997, Cholinesterase.
	DR	InterPro, IPR00379, Ser_estrs.
	DR	Pfam, PF00135, Coesterase_1.
	DR	PRINTS, PR00878, CHOLNESTRASE.
	DR	PROSITE, PS00122; CARBOXYLESTERASE_B_1; 1.
	DR	PROSITE, PS00941; CARBOXYLESTERASE_E_2; 1.
	KM	3D-structure; Alternative splicing; Blood group antigen; Direct protein sequencing; Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation; Polymorphism; Serine esterase; Signal; Synapse.
	KX	SYNAPSE.
	FT	SIGNAL 1 31 Potential.
	FT	CHAIN 32 614 Acetylcholinesterase.
	FT	ACT_SITE 234 234 Acyl-ester intermediate.
	FT	ACT_SITE 365 365 Charge relay system.
	FT	ACT_SITE 478 478 Charge relay system.
	FT	DISULFD 100 127 Interchain.
	FT	DISULFD 288 303 Disulfide bond.
	FT	DISULFD 440 560 Disulfide bond.
	FT	DISULFD 611 611 Disulfide bond.
	FT	CARBOND 296 296 N-linked (GlcNAc...) (Potential).
	FT	CARBOND 381 381 N-linked (GlcNAc...) (Potential).
	FT	CARBOND 495 495 DTT-sensitive site.
	FT	VASPLIC 575 614 --> GMPGNAGRGVGAQCNPGLPPLAEPASTCPGR HGSAFRPG...LPDLLHLLFLSHLRRL (in isoform 2).
	FT	/Fld=VSP_001457. V->E (in dbSNP:8286). /Fld=VAR_011934. H->N (in Yt(b)) antigen; dbSNP:1799605). /Fld=VAR_002359.
	FT	VARIANT 353 353
	FT	VARIANT 353 353
	FT	

FT MUTAGEN 206 206 D->N: Misfolding, absence of secretion.
 FT MUTAGEN 234 234 S->A: Loss of activity.
 FT MUTAGEN 365 365 E->A: Loss of activity.
 FT MUTAGEN 435 435 D->N: Misfolding, absence of secretion.
 FT MUTAGEN 478 478 H->A: Loss of activity.
 FT MUTAGEN 611 611 C->A: Impairment of interchain disulfide bridge formation.
 FT TURN 38 39
 FT STRAND 40 42
 FT STRAND 47 49
 FT STRAND 51 53
 FT TURN 56 57
 FT STRAND 60 67
 FT STRAND 69 70
 FT HELIX 74 76
 FT TURN 77 78
 FT STRAND 82 83
 FT STRAND 90 92
 FT STRAND 94 94
 FT STRAND 99 100
 FT TURN 109 110
 FT HELIX 112 115
 FT TURN 116 117
 FT STRAND 123 124
 FT STRAND 129 135

Query Match 52.1%; Score 1698.5; DB 1; Length 614;
 Best Local Similarity 52.3%; Pred. No. 3.8e-119;
 Matches 312; Conservative 106; Mismatches 167; Indels 11; Gaps 6;

QY 17 LLLCML---IGKSHED-DIIATKNGKVRGNLTVFGGTVAFAGIPIYAOPPLGRLEFK 72
 DB 20 LLLMLGGGVAEGREDELIVYRGKRLKRTGGPVSALGIPPAEPMPRRFL 79
 QY 73 KPSLTKMSDIMNATKYANSCCONIDSPFGHSGEMNNTDLSBDCLYLWVTPARKP 132
 DB 80 PPEPKQPMGVDATTFQGVCYQYVDLTPGEGTEMNPNRELSEBDCLYLWVTPYPRP 139
 QY 133 KNAT-VLIWYGGGFQGTSSILHYDGFARVERIVVSNMYRGALGFALPGNPEAP 191
 DB 140 TSPPTVLWVIYGGGFYSAGSSLDVYDGRFLVQAEETVLVSNMYRGALGFALPGSREAP 199
 QY 192 GNMGLPQOALQWVQKNIIAFGNPKSVTLFGESAGAAVSLLHLSPGSHSLFTRAILQ 251
 DB 200 GNVGLDQRLALQWQENVAAGFDPSTVTLFGESAGAAVSVMHLSPPSGLFHRAVLQ 259
 QY 252 SGSFNAFWAVTSLYEARNFTLAKLTGC---SRNETEIIKLCRNKDPQELINAEFV 307
 DB 260 SGAPNGPMAVTVGMEARRRATQLAHLVGCPPGTGNDTELVACLTRPAQVLVNHMHV 319
 QY 308 VVYGPPLSNPPTVDGDELTPMDILLLEAGFKTQILVGVNKDEGTWFLVYGAFGFSK 367
 DB 320 LPOESVFRFSFVVDGDLSDTPEALINAGDFHGLQVLVGVYKDEGSYFLVYGAFGFSK 379
 QY 368 DNNSIITRKEFOGLKIFPPGVSEFGKESILFHYTDVDDQRPENYREALGVGDYNYFI 427
 DB 380 DNESLISRBEFLAGRVGVQVSDLAABAVALHYTDLHEDPALREALSDVGDHNVV 439
 QY 428 CPALFTKPSSEWGNNAFFYYFEHRSKLPWPMGMGMGEYIEFVGLPIERRDYTTKA 487
 DB 440 CPVAQLAGRLAQAQARVYAVYFEHRASTLSWPLMGVPHGEYIEFVGLPIERDPSRNYTAE 499
 QY 488 EELLSISYRMANFAKYNPNETON-NSTSWPFVKTEQKYLTLNTESTRIITLKLRAQ 546
 DB 500 EKLFARLKYMANFAKRTGDPNPPPKAPQMPPTYAGAQQVYSIDRLERARRGRLAQA 559
 QY 547 CRFTWTFEPKYLEMTGNIDAEWEMWKAFFHRANNYMDWKNQFNQDYTSKESCVGL 602
 DB 560 CAMWNFPLKTLATDTLDEARQMKAEFRHMSYVHWKNOFDHY-SKQDCSDL 614

RESULT 15
 AAP22365

ID AAP22365 PRELIMINARY; PRT; 614 AA.
 AC AAP22365;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein ACHE.
 GN ACHE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99063792; PubMed=9847074;
 RX Wilson R.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Drone K., Lapiant Y., Nguyen C., Reitz L., Sun H.;
 RT "The sequence of Homo sapiens BAC clone RP11-12615.";
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AC011895; AAP22365.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67796 MW; B9AA84C77831C302 CRC64;

Query Match 52.1%; Score 1698.5; DB 2; Length 614;
 Best Local Similarity 52.3%; Pred. No. 3.8e-119;
 Matches 312; Conservative 106; Mismatches 167; Indels 11; Gaps 6;

QY 17 LLLCML---IGKSHED-DIIATKNGKVRGNLTVFGGTVAFAGIPIYAOPPLGRLEFK 72
 DB 20 LLLMLGGGVAEGREDELIVYRGKRLKRTGGPVSALGIPPAEPMPRRFL 79
 QY 73 KPSLTKMSDIMNATKYANSCCONIDSPFGHSGEMNNTDLSBDCLYLWVTPARKP 132
 DB 80 PPEPKQPMGVDATTFQGVCYQYVDLTPGEGTEMNPNRELSEBDCLYLWVTPYPRP 139
 QY 133 KNAT-VLIWYGGGFQGTSSILHYDGFARVERIVVSNMYRGALGFALPGNPEAP 191
 DB 140 TSPPTVLWVIYGGGFYSAGSSLDVYDGRFLVQAEETVLVSNMYRGALGFALPGSREAP 199
 QY 192 GNMGLPQOALQWVQKNIIAFGNPKSVTLFGESAGAAVSLLHLSPGSHSLFTRAILQ 251
 DB 200 GNVGLDQRLALQWQENVAAGFDPSTVTLFGESAGAAVSVMHLSPPSGLFHRAVLQ 259
 QY 252 SGSFNAFWAVTSLYEARNFTLAKLTGC---SRNETEIIKLCRNKDPQELINAEFV 307
 DB 260 SGAPNGPMAVTVGMEARRRATQLAHLVGCPPGTGNDTELVACLTRPAQVLVNHMHV 319
 QY 308 VVYGPPLSNPPTVDGDELTPMDILLLEAGFKTQILVGVNKDEGTWFLVYGAFGFSK 367
 DB 320 LPOESVFRFSFVVDGDLSDTPEALINAGDFHGLQVLVGVYKDEGSYFLVYGAFGFSK 379
 QY 368 DNNSIITRKEFOGLKIFPPGVSEFGKESILFHYTDVDDQRPENYREALGVGDYNYFI 427
 DB 380 DNESLISRBEFLAGRVGVQVSDLAABAVALHYTDLHEDPALREALSDVGDHNVV 439
 QY 428 CPALFTKPSSEWGNNAFFYYFEHRSKLPWPMGMGMGEYIEFVGLPIERRDYTTKA 487
 DB 440 CPVAQLAGRLAQAQARVYAVYFEHRASTLSWPLMGVPHGEYIEFVGLPIERDPSRNYTAE 499

Db 559 TCAPMRPFLDKLSDITDLEDRQKAFHRNMSYMKVQFPHY-SKGRCSDL 614

RESULT 17
ACCS_MOUSE STANDARD; PRT; 614 AA.
ID ACES_MOUSE
AC P21836;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name:ACHE;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90380429; PubMed=240605;
RX RACHINSKY T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species".
RL Neuron 5:317-327(1990).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RX MEDLINE=21139439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schumpf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TRP2 region on human
chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL Nucleic Acids Res. 29:1352-1365(2001).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=retina;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuld S.P., Zeeberg B., Buetow K.H., Scheffer C.F., Hsieh P.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smilins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN INTERACTION WITH PRIMA1.
RP MEDLINE=21664287; PubMed=11804574;
RX Perrier A.L., Massoulié J., Krejci E.;
RT "PRIMA1, the membrane anchor of acetylcholinesterase in the brain.";
RL Neuron 33:275-285(2002).
[5]
RN X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RP MEDLINE=96067648; PubMed=8521480;
RX Bourne Y., Taylor P., Marchot P.;
RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
the complex.";
RL Cell 83:503-512(1995).
[6]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

RX MEDLINE=99115643; PubMed=9915834;
RA Bourne Y., Taylor P., Bougie P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
occluding loop in a tetrameric assembly.";
RL J. Biol. Chem. 274:2963-2970(1999).
[7]
RN X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 34-573 IN COMPLEX WITH
RP INHIBITOR.
RX PubMed=12505979; DOI=10.1093/embio/cdg005;
RA Bourne Y., Taylor P., Radic Z., Marchot P.;
RT "Structural insights into ligand interactions at the
acetylcholinesterase peripheral anionic site.";
RL EMBO J. 22:1-12(2003).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Isoform H generates GPI-anchored dimers; disulfide
CC linked. Isoform T generates multiple structures, ranging from
CC monomers and dimers to collagen-tailed and hydrophobic-tailed
CC forms, in which catalytic tetramers are associated with anchoring
CC proteins that attach them to the basal lamina or to cell
CC membranes. In the collagen-tailed forms, isoform T subunits are
CC associated with a specific collagen, COLQ, which triggers the
CC formation of isoform T tetramers, from monomers and dimers (by
CC similarity). Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=P21836-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P21836-2; Sequence=Not described;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Predominant in most expressing tissues except
CC erythrocytes where a glycopospholipid-attached form of AChE
CC predominates.
CC -1- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
CC cholinesterase, with a collagen-like part disulfide-bonded to the
CC catalytic part. A different, globular type of cholinesterase
CC occurs on the outer surfaces of cell membranes, including those of
CC erythrocytes.
CC -1- MISCELLANEOUS: This is the catalytic subunit of an asymmetric or
CC soluble form of AChE.
CC -1- SOLUBLE FORM OF AChE.
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CC entities requires a license agreement (See <http://www.isb-stb.ch/announce/>
CC or send an email to license@isb-stb.ch).
CC -----
CC EMBL; X56518; CA39867.1; -;
CC EMBL; AF312033; AA28816.1; -;
CC EMBL; BC046327; AA46327.1; -;
CC PIR; JH0314; JH0314.
CC PDB; 1C2B; X-ray; A=35-573.
CC PDB; 1C2O; X-ray; A/B/C/D=36-574.
CC PDB; 1J06; X-ray; A/B=32-574.
CC PDB; 1J07; X-ray; A/B=32-574.
CC PDB; 1K06; X-ray; A=32-580.
CC PDB; 1MAA; X-ray; A/B/C/D=32-578.
CC PDB; 1MAH; X-ray; A=32-574.
CC PDB; 1NSM; X-ray; A/B=32-572.
CC PDB; 1NSR; X-ray; A/B=32-574.
CC PDB; 1O83; X-ray; A/B=1-580.
CC MGD; MGI:87876; Ache.
CC GO; GO:0045202; C:synapse; IDA.
CC InterPro; IPR002018; Cholinesterase.
CC InterPro; IPR000379; Ser_estr.
CC Pfam; PF00135; Coesterase; 1.

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohata N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK043748; BAC31641.1; -
 SO SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;
 Query Match 51.9%; Score 1692.5; DB 2; Length 614;
 Best Local Similarity 52.1%; Pred. No. 1.1e-118;
 Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;
 QY 10 IRLFWFLLLCMLIGKSHTE---DDIIIAKNGKVGMLTVGRTVTAFLGIPVYQPP 65
 DB 13 LAFPLFLSLGCGARBEREDPQLVRVGGQLKIRKADGEPVSAVLGIPVAPP 72
 QY 66 LGLRLFKPKPOLITGMSDINWATKYANSCQNIIDSPFGFHSSEMNPTDISEDCILNV 125
 DB 73 VGSRRFPKPKRWSGVLDATTQNCYQVVDLYGFEFETEMNNRREISECTILNV 132
 QY 126 WIPAPKPKNAT-VLIWYGGGFGTGTSSLHVYDGKFLARVERVIVSMYRVGALGLAL 184
 DB 133 WTPYRPASPTPLVLIWYGGFGYGAASLDVYDGRFLAQLVGVSMYRVGFGFLAL 192
 QY 185 PGNPBEAGMGLPPOQALWQVQNTIAFGNPKSVTLFPGSAGAAVSLSLSPGSHL 244
 DB 193 PGSEAEAGNVGLLDQRLALWQVQNTIAFGDPMSTVTLFPGSAGAAVSLSLSPRSL 252
 QY 245 FTBALDGSFNAFWATSLYEANRTILAKLTGC---SREVTETIKCLRKMDQEI 300
 DB 253 FHRVAVLOSCTPNGWMAVTSAGEARRRATLALVGCPCGAGAGDTIELICLRPPADL 312
 QY 301 LNEAFVVPYGTPLSVNFGPTVDDFTLMDLILLEGQFKKTQILVGNKDEGTWFLVY 360
 DB 313 VDHEWHTLPQESIFRPSFVPVVDGDFLSDPFEALINTGDFODLQVLGVVDEGSYFLVY 372
 QY 361 GAREFSQDNNSIIRKPFQEBGLKFPFGVSFPGESILFHTWVDQRPNTYREALGDV 420
 DB 373 GVPEFSQDNSSLISRAQFLAGVRIGVQASDLAEAVLHTDMLHEDPFLHLDASAV 432
 QY 421 VGDVNFICPALFETKSEWGNNAFFYFPEHRSKCLPMEWGMGWHGEIEFVGLPLER 480
 DB 433 VGDHNVCPVAQLAGRLAAGARVYATIFERASTLWPLMGVPRHGEIEFVGLPLDP 492
 QY 481 RDNVTKAEILSRGIVRMANFAKYGNPNTQNN-STSPVFKSTBEKYLTLNTESTRIM 539
 DB 493 SLNVTTERIFAQGLMKYMTVFATGDPNDPDSKSPQWPRYTTAAQYVSLNKLPLEVR 552
 QY 540 TKLRAGQCRWTSFPFVLENTGNIDAEWENKAGFRMNNYMDKQGFNDYSKESK 599
 DB 553 RGLRAQCAFWNRLPKLLSATDTLDEARQWKAFFRWSSYVWVWKNQPDHY-SKQERC 611
 QY 600 VGL 602
 DB 612 SDL 614

BAC32595
 ID BAC32595 PRELIMINARY; PRT; 614 AA.
 AC BAC32595;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
 DE library, clone:B203040L13 product:acetylcholinesterase, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akimura T., Nishi K., Kitsuai T., Taahiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kasaiwaagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohata N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RESULT 20

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK046080; BAC32595.1; -
 SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;
 Query Match 51.9%; Score 1692.5; DB 2; Length 614;
 Best Local Similarity 52.1%; Pred. No. 1.1e-118;
 Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;
 10 IRELFWFLLCMLIGKSHTE---DIIITATKNGKRGKGNLTVFGGTATFAGIPYAPAP 65
 13 LARPLFLILLISGGGARBARGBEDPQLTVVRGGQLRGIRLKA PGGVSAFLGIPEAPRP 72
 66 LGRIRFKKPSLTYSMDIWMATKANSCCNIDQSPFGFGSEMPMNTDLSDCILYANV 125
 73 VGSRRFMPPEPKRPMGSGVLDATTFQNVCYQYVDTLVFGFGTGMNPNRSLSDCYLANV 132
 126 WIPAPRKKNAT-VLITWYGGGFGTGTSLHYVDGKFLARVERVYVVMRYVALGFLAL 184
 133 WTPYPRPASFTPLVIMWYGGGFYSGAASLDVYDGRFLAQVEGAVISMRYVGTGFLAL 192
 185 PGNEPABGNMGLPDQOLALQWVQKNIAGFGNPKSVTLFSESAGASVSILHLSPGSHL 244
 193 PGSEAPAGNVGLDQRLALQWQENIAAFGDPMSVTLFSESAGASVGMHILSLPSRL 252
 245 FTRAILLOGSPNAPWATSLYEAKRRLINAKLTGC---SREMETEIKICLNKQPOEI 300
 253 FHRVLTOSGTNGPMATVSGEARRRATLLARLVGCPGAGGNDTELICLRTRPADL 312
 301 LILNAFVVPYGTPTSVNFGFTVDGFTLDMFDILLEGOFKTQILVGNKDEGTWFLVY 360
 313 VDHENWVLPQESIRFPGFVPPVDDFLSDTPEALINQDGDQVLVGVKDESGYFLVY 372
 361 GAGPFSKDNNSITRKEFGSLKTFPGVSEFGKSLIFHTWVDVDORENTREALGDV 420
 373 GVPGFSKDNESLISRAQFLAGVIRIGVQASDLAEAVLHTDMLHEDDPHLEADMSAV 432
 421 VGDVNFICPALEFFKKSEMNNAFFYFEHRSKSLMPMEMGMVHGGEIEFVGLPLER 480
 433 VGDHNVCPVQAQLAGRLAQAARVAYAFERRASTLWPLMVGPHGVEIEFICGLDLP 492
 481 RDNVTKAEILSRISIKWANFAKYNENETONN-STSWPVFKSTEOXYTLTNTSETRIM 539
 493 SLNTTTERIPAQLMKMTWTFARTGDPNDPRDSKPCWPYTTAAQYVSLNKPLEVR 552
 540 TKLRQAQCRFTSPFPKYLENTGNIDEMEMKACFHRNNYMDKQFNDYSSKESC 599
 553 RGLRAQTCAPWNRFLPKLLSATDITLDEARQMKAEFHRSSSYVMWKNQFDHY-SKQERC 611
 600 VGL 602
 612 SDL 614
 RESULT 21
 ACES_FELCA STANDARD; PRT; 611 AA.
 ID ACES_FELCA
 AC 062763; 062762;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 01-OCT-2004 (Rel. 45; Last annotation update)
 DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
 GN Name=ACHE;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Carnivora; Fissipedia; Felidae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=20334351; PubMed=10874122;
 RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
 RA Lockridge O.;
 RT "determination of the DNA sequences of acetylcholinesterase and
 butyrylcholinesterase from cat and demonstration of the existence of

RT both in cat plasma";
 RL Biochem. Pharmacol. 60:479-487(2000).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H₂O = choline + acetate.
 CC -1- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
 CC required to anchor it to the basal lamina of cells and organize
 CC into tetramers (By similarity). Isoform H generates GPI-anchored
 CC dimers; disulfide linked. Isoform T generates multiple structures,
 CC ranging from monomers and dimers to collagen-tailed and
 CC hydrophobic-tailed forms, in which catalytic tetramers are
 CC associated with anchoring proteins that attach them to the basal
 CC lamina or to cell membranes. In the collagen-tailed forms, isoform
 CC T subunits are associated with a specific collagen, COL4, which
 CC triggers the formation of isoform T tetramers, from monomers and
 CC dimers.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=T;
 CC IsoId=O62763-1; Sequence=Displayed;
 CC Name=H;
 CC IsoId=O62763-2; Sequence=VSP_001456;
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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 CC
 DR EMBL; AF053485; AAC08995.1; -
 DR EMBL; AF053485; AAC08996.1; -
 DR HSSP; P22303; 1F8U.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000379; Cholinesterase.
 DR InterPro; IPR000379; Ser. esters.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTERASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
 DR PROSITE; PS00941; GLYCOPROTEIN Hydrolase; Membrane;
 DR Alternative splicing; Glycoprotein; Hydrolase;
 DR Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 DR
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
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Db	140	TPVLVMTYGGGFTSGASSLVDYDGRLLDAGECTVLSNMNYVGAAGFLTAGSEAAQNV	199
Qy	195	GLFDDOLALQWYOKNIAAFQGNPKSVTLFGEASAGASVSLHLSPGSHSLFTRAILQGS	254
Db	200	GLDDQRLALQWQDVNAVTFGSDPMVSTLFGESAGAASTVGMHLSPSGKLFHRAVLQSGA	259
Qy	255	FNAPMAVTSLEYARNRTLMAKLTGC---SKENETELIKCLRNKDPEILNANAPVVPY	310
Db	260	PNBPMAVTVGGEARRRATLLARIYVCGPPGAGAGNDTELVALCRRRPADLDVHSMHVLPO	319
Qy	311	GTELSAVNFGPTVVDGDELTMDDILLETGQFKKTQILLVGNKDEGTWFLVYGAPEFSKDN	370
Db	320	ESVFRFSFVYVDGDLSTDPETALINAGDFHQLQVLVGVYDDEGSLFLVYGAPEFSKDNE	379
Qy	371	SITTRKEPQEGKIIPPVGVSEFKESILFHYTDWVDQRPENYREALGDVVDYNTCPA	430
Db	380	SLTSRAQFLAGVYVGPQASDLAAEAVVLYHTYDMINLPEDPARLEAMSDVVDHNVCPV	439
Qy	431	LEETKFKFSEMGNNAPFYVFEHRSSTLPMDEMGVNHGEIPEVETLPERDNTAKXEI	490
Db	440	AQLAGRIAAQGANVYVIFEHRSSTLSWLMGVHGEIETLPELPEPSLNTAERI	499
Qy	491	LSRSIVKRWANFAKYNPNPETOINNST-SWPKVKSTEQVLTILINESTRIMTKLAAQOCRF	549
Db	500	FAQRLRWYMANFARTQDPPNDPDKVQCPPTAYGAQQYVSLDRPLEVRGRGLAAQCAF	559
Qy	550	WTSPFPKVLTEMTGNIDAEWEMKACGHRNRNNYMDMKQOFNDYTSKSSCYGL	602
Db	560	WNFFLPLGLSATYTLDEARQWAAEHRASSTVYMWKQOFHY-SKQRCSDL	611

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RESULT 22
09GKJ6
ID 09GKJ6 PRELIMINARY; PRT; 349 AA.
AC 09GKJ6;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase (Fragment).
GN Name=BChE;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419000; Pubmed=11528129;
RA Van Poucke M., Yerie M., Tugayle C., Piumi F., Genet C.,
RA Van Zeveren A., Peelman L.J.;
RT "Integration of porcine chromosome 13 maps.";
RL Cytogenet. Cell Genet. 93:297-303(2001).
CC 1-1 SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.
DR EMBL, AF222814; M041127.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0004104; F: cholinesterase activity; IEA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser_estrb.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1, 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 349 AA; 39061 MW; D66354B14725BE58 CRC64;

Query Match 51.3%; Score 1674; DB 2; Length 349;
Best Local Similarity 91.4%; Pred. No. 1,2e-117;
Matches 319; Conservative 6; Mismatches 24; Indels 0; Gaps 0

141 TGGGFGTGTGSSLAHYDQKFLARVEYIVSNRVRGALGFLALPQNPAAQNGGLFDQO

```

Db	1	IVGGGQTGTSSLHYVDGKFLSRVERVIVVSMNRRVGLAGLALPGNPEARGNNGLPDDQ	60
Qy	1201	LALQWQKRIIAAPGNPKSVTLFGSSAQAASVSLHLSPGSHSLFTRAILQSSGFNAPMA	260
Db	61	LALQWQKRIIAAPGNPKSVTLFGSSAQAASVSLHLSPKSHPLPABAILQSSGNAPMA	120
Qy	261	VTSLYEARRRITLNAKTGCSRRENTETIKCLRNKDPOELLINBAFVVPYPTPLSVNFGP	320
Db	121	VTSLYEARRRITLNAKFGCSRRENTETIKCLRNNDPQELLQNVFVVPNNMLLSVNFGR	180
Qy	321	TVVGDDELTMPPDILLETGQPKKTOILVNVNDEGFWLVYGAPEPFSKDNNSIITRKEFOE	380
Db	181	TVVGDDELTPDILLQGGPKKTQLLVANVNDGFAISVYGAPEFSKDNNSIITRKEFE	240
Qy	381	GLKIFPFGVSEFGKESILFHYTDWVDORPENRYEALDDVGDYNFICPALFPTKSEW	440
Db	241	GLKIFPFGVSEFGKESILFHYMDWTDORAEVYRDALDDVGDYDIIICPALFPTKSEW	300
Qy	441	GNNAPFYFVFEHRSKLPMPWEMGVNHGEIFPVGLPIERDNTTKAE	489
Db	301	GNNAPFYFVFEHRSKLPMPWEMGVNHGEIEFVGLPIERRANTTKAE	349

```

RESULT 23
ACCS_BOVIN STANDARD; PRT; 613 AA.
ID ACES_BOVIN P23795;
AC P23795; 097579;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN Name=ACHE;
OS Bos taurus (Bovine).
OC Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Kidney;
RC MEDLINE=98539754; PubMed=9693127;
RA Mendelson I., Kroman C., Ariel N., Shafferman A., Velan B.;
RT "Bovine acetylcholinesterase: cloning, expression and
RT characterization";
RL Biochem. J. 334:251-259(1998).
[2]
RN SEQUENCE OF 31-613 (ISOFORM H).
RP TISSUE=Fetal serum;
RC MEDLINE=90306335; PubMed=2365060;
RX Doctor B.P., Chapman T.C., Christler C.E., Deal C.D., de la Hoz D.M.,
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
RT "Complete amino acid sequence of fetal bovine serum
RT acetylcholinesterase and its comparison in various regions with other
RT cholinesterases.";
RL FEBS Lett. 266:123-127(1990).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organize
CC into tetramers (By similarity). Isoform H generates GPI-anchored
CC dimers; disulfide linked. Isoform T generates multiple structures,
CC ranging from monomers and dimers to collagen-tailed and
CC hydrophobic-tailed forms, in which catalytic tetramers are
CC associated with anchoring proteins that attach them to the basal
CC lamina or to cell membranes. In the collagen-tailed forms, isoform
CC T subunits are associated with a specific collagen, COL4, which
CC triggers the formation of isoform T tetramers, from monomers and
CC dimers.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=P23795-1; Sequence=Displayed;
CC Name=H;

```


RA Taylor S.S., Taylor P.;
 RT "Divergence in primary structure between the molecular forms of
 RT acetylcholinesterase.";
 RL J. Biol. Chem. 263:1140-1145(1988).
 RN [6]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=90166618; PubMed=2306366;
 RA Malet Y., Camp S., Gibney G., Rachinsky T.L., Ekstrom T.J.,
 RA Taylor P.;
 RT "Single gene encodes glycopospholipid-anchored and asymmetric
 RT acetylcholinesterase forms: alternative coding exons contain inverted
 RT repeat sequences.";
 RL Neuron 4:289-301(1990).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=87008586; PubMed=3759980;
 RA McPhee-Quigley K., Vedrick T.S., Taylor P., Taylor S.S.;
 RT "Profile of the disulfide bonds in acetylcholinesterase.";
 RL J. Biol. Chem. 261:13565-13570(1986).
 RN [8]
 RP STRUCTURE OF THE GPI-ANCHOR.
 RX MEDLINE=94079692; PubMed=8257440;
 RA Mehler A., Varon L., Silman I., Homans S.W., Ferguson M.A.;
 RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of
 RT acetylcholinesterase from the electric organ of the electric fish,
 RT Torpedo californica.";
 RL Biochem. J. 296:473-479(1993).
 RN [9]
 RP GPI-ANCHOR.
 RX MEDLINE=96176849; PubMed=8597567; DOI=10.1016/0167-4838(95)00205-7;
 RA Bucht G., Hjalmarsson K.;
 RT "Residues in Torpedo californica acetylcholinesterase necessary for
 RT processing to a glycosyl phosphatidylinositol-anchored form.";
 RL Biochim. Biophys. Acta 1252:223-232(1996).
 RN [10]
 RP MOTAGENESIS.
 RX MEDLINE=91017542; PubMed=2217185;
 RA Gibney G., Camp S., Dionne M., McPhee-Quigley K., Taylor P.;
 RT "Mutagenesis of essential functional residues in
 RT acetylcholinesterase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=91343928; PubMed=1678899;
 RA Susman J.L., Harel M., Frolow F., Oefner C., Goldman A., Tokar L.,
 RA Silman I.;
 RT "Atomic structure of acetylcholinesterase from Torpedo californica: a
 RT prototypic acetylcholine-binding protein.";
 RL Science 253:872-879(1991).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE=96366673; PubMed=8747462;
 RA Harel M., Klewegt G.J., Raveill R.B., Silman I., Susman J.L.;
 RT "Crystal structure of an acetylcholinesterase-fasciculin complex:
 RT interaction of a three-fingered toxin from snake venom with its
 RT target.";
 RL Structure 3:1355-1366(1995).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=97143314; PubMed=8989325;
 RA Raves M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,
 RA Susman J.L.;
 RT "Structure of acetylcholinesterase complexed with the nootropic
 RT alkaloid, (-)-huperzine A.";
 RL Nat. Struct. Biol. 4:57-63(1997).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=99249780; PubMed=10231521;
 RA Bartolucci C., Perola E., Cellai L., Brufani M., Lamba D.;
 RT "Back door" opening implied by the crystal structure of a
 RT carbamoylated acetylcholinesterase.";
 RL Biochemistry 38:5714-5719(1999).
 RN [15]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=99282167; PubMed=10353814;
 RA Millard C.B., Kryger G., Ordentlich A., Greenblatt H.M., Harel M.,
 RA Raves M.L., Segall Y., Barak D., Shaferman A., Silman I.,
 RA Susman J.L.;
 RT "Crystal structures of aged phosphorylated acetylcholinesterase: nerve
 RT agent reaction products at the atomic level.";
 RL Biochemistry 38:7032-7039(1999).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=20074924; PubMed=10606746;
 RA Greenblatt H.M., Kryger G., Lewis T., Silman I., Susman J.L.;
 RT "Structure of acetylcholinesterase complexed with (-)-galanthamine at
 RT 2.3-A resolution.";
 RL FEBS Lett. 463:321-326(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=99197295; PubMed=10368299;
 RA Kryger G., Silman I., Susman J.L.;
 RT "Structure of acetylcholinesterase complexed with E2020 (Aricept(R)):
 RT implications for the design of new anti-alzheimer drugs.";
 RL Structure 7:297-307(1999).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC May be involved in cell-cell interactions.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: The H form is an homodimer; the asymmetric form is a
 CC disulfide-bonded oligomer composed of a collagenic subunit (Q) and
 CC a variable number of T catalytic subunits.
 CC -1- SUBCELLULAR LOCATION: The H form is attached to the membrane by a
 CC GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=H; Synonyms=Globular;
 CC IsoId=P04058-1; Sequence=displayed;
 CC Name=T;
 CC IsoId=P04058-2; Sequence=VSP_001460;
 CC -1- TISSUE SPECIFICITY: Found in the synapses and to a lower extent in
 CC extrajunctional areas of muscle and nerve, and on erythrocyte
 CC membranes.
 CC -1- PTM: An interchain disulfide bond is present in what becomes
 CC position 593 of the T isoform.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; X03439; CA27169.1; -;
 CC EMBL; X56516; -; NOT ANNOTATED_CDS.
 CC EMBL; X56517; -; NOT ANNOTATED_CDS.
 CC PIR; A00773; ACRYE.
 DR PDB; 1ACJ; X-ray; @=22-558.
 DR PDB; 1ACU; X-ray; @=22-558.
 DR PDB; 1AMN; X-ray; @=22-558.
 DR PDB; 1AXJ; X-ray; @=22-558.
 DR PDB; 1CFJ; X-ray; A=22-558.
 DR PDB; 1DX6; X-ray; A=22-564.
 DR PDB; 1E3Q; X-ray; A=22-564.
 DR PDB; 1E66; X-ray; A=22-564.
 DR PDB; 1E67; X-ray; A=22-564.
 DR PDB; 1EA5; X-ray; A=22-558.
 DR PDB; 1EBA; X-ray; A=22-555.
 DR PDB; 1EVE; X-ray; @=22-564.
 DR PDB; 1FSS; X-ray; A=22-558.
 DR PDB; 1GPN; X-ray; A=22-558.
 DR PDB; 1GPR; X-ray; A=22-558.
 DR PDB; 1GQR; X-ray; A=25-556.
 DR PDB; 1GQS; X-ray; A=25-556.
 DR PDB; 1H22; X-ray; A=22-564.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:28:32 ; Search time 43 Seconds
(without alignments)
1347.035 Million cell updates/sec

Title: us-09-748-739a-2

Perfect score: 3260
Sequence: 1 MDSKVITICIRFLFWLLLC.....MDKKNQFNQDYTSKKESCVGL 602

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3239	99.4	602	1	ACHU
2	2855.5	87.6	581	2	cholinesterase (EC
3	2593	79.5	603	1	cholinesterase (EC
4	1791.5	55.0	596	1	cholinesterase (EC
5	1789.5	54.9	599	1	cholinesterase (EC
6	1698.5	52.1	614	2	cholinesterase (EC
7	1693.5	51.9	614	2	cholinesterase (EC
8	1692.5	51.9	614	2	cholinesterase (EC
9	1639	50.3	584	2	cholinesterase (EC
10	1636.5	50.2	583	2	cholinesterase (EC
11	1466	45.0	767	2	cholinesterase (EC
12	1142	35.0	620	2	cholinesterase (EC
13	1075.5	33.0	637	2	cholinesterase (EC
14	1045	32.1	691	2	cholinesterase (EC
15	1044	32.0	746	2	cholinesterase (EC
16	1038.5	31.9	664	2	cholinesterase (EC
17	1025.5	31.5	602	2	cholinesterase (EC
18	951	29.2	629	2	cholinesterase (EC
19	937	28.7	584	2	cholinesterase (EC
20	930	28.5	607	2	cholinesterase (EC
21	893	27.4	532	2	cholinesterase (EC
22	754	23.1	532	2	cholinesterase (EC
23	753	22.7	559	2	cholinesterase (EC
24	740.5	22.5	559	2	cholinesterase (EC
25	733	22.4	551	2	cholinesterase (EC
26	731.5	22.4	597	2	cholinesterase (EC
27	729	22.3	612	2	cholinesterase (EC
28	727	22.2	554	2	cholinesterase (EC
29	724.5	22.2	554	2	cholinesterase (EC

30	724	22.2	141	2	D39768	cholinesterase (EC
31	721	22.1	141	2	F39768	cholinesterase (EC
32	721	22.1	141	2	B39768	cholinesterase (EC
33	716	22.0	565	2	S10367	cholinesterase (EC
34	713.5	21.9	562	2	A55281	cholinesterase (EC
35	711	21.8	745	2	S13586	cholinesterase (EC
36	707	21.7	141	2	E39768	cholinesterase (EC
37	701.5	21.5	557	2	A47162	cholinesterase B (E
38	700.5	21.5	567	2	A41010	cholinesterase (EC
39	700	21.5	561	2	JC2447	cholinesterase (EC
40	699.5	21.5	549	2	JX0054	cholinesterase (EC
41	697	21.4	540	2	A31584	cholinesterase (EC
42	692	21.2	561	2	S62788	cholinesterase (EC
43	691	21.2	561	2	S71597	cholinesterase (EC
44	690.5	21.2	566	2	S19307	cholinesterase (EC
45	666	20.4	556	2	A56920	cholinesterase (EC
46	656.5	20.1	554	1	S34607	cholinesterase (EC
47	649	19.9	540	2	S51043	cholinesterase (EC
48	636	19.5	2769	1	UIBO	cholinesterase (EC
49	632.5	19.4	967	1	UIRT	cholinesterase (EC
50	627	19.2	540	2	A75250	cholinesterase (EC
51	624	19.1	593	1	S25062	cholinesterase (EC
52	620	19.0	539	2	A29923	cholinesterase (EC
53	604	18.5	2767	1	UIHU	cholinesterase (EC
54	603.5	18.5	562	2	S27782	cholinesterase (EC
55	599.5	18.4	564	1	S36787	cholinesterase (EC
56	594	18.2	489	1	B69680	cholinesterase (EC
57	589.5	18.1	583	2	T25690	cholinesterase (EC
58	587.5	18.0	582	2	S34786	cholinesterase (EC
59	585	17.9	506	2	H75522	cholinesterase (EC
60	585	17.9	554	2	T31783	cholinesterase (EC
61	585	17.9	557	2	A56690	cholinesterase (EC
62	574.5	17.6	564	2	T28949	cholinesterase (EC
63	556	17.1	547	2	T29717	cholinesterase (EC
64	554.5	17.0	562	2	S27800	cholinesterase (EC
65	553	17.0	568	2	T32807	cholinesterase (EC
66	548.5	16.8	550	1	A34576	cholinesterase (EC
67	540.5	16.6	570	2	T32061	cholinesterase (EC
68	538.5	16.5	730	2	T16455	cholinesterase (EC
69	534.5	16.4	578	2	F89068	cholinesterase (EC
70	534.5	16.4	578	2	F89068	cholinesterase (EC
71	531.5	16.3	502	2	A60666	cholinesterase (EC
72	526	16.1	543	2	T27000	cholinesterase (EC
73	522.5	16.0	798	2	T19864	cholinesterase (EC
74	522	16.0	565	2	T29718	cholinesterase (EC
75	520.5	16.0	545	2	A89046	cholinesterase (EC
76	520	16.0	535	2	B34576	cholinesterase (EC
77	520	16.0	535	2	A35986	cholinesterase (EC
78	512	15.7	540	2	S53571	cholinesterase (EC
79	510	15.6	571	2	G89123	cholinesterase (EC
80	508	15.6	540	2	S53370	cholinesterase (EC
81	501.5	15.4	578	2	B89045	cholinesterase (EC
82	497	15.2	549	2	UN0552	cholinesterase (EC
83	491	15.1	433	2	G89045	cholinesterase (EC
84	490.5	15.0	544	2	A34325	cholinesterase (EC
85	490	15.0	544	2	B40122	cholinesterase (EC
86	490	15.0	544	2	A41426	cholinesterase (EC
87	490	15.0	544	2	A34089	cholinesterase (EC
88	490	15.0	548	2	A28022	cholinesterase (EC
89	489	15.0	544	2	C41426	cholinesterase (EC
90	485	14.9	544	2	D41426	cholinesterase (EC
91	485	14.9	544	2	A41426	cholinesterase (EC
92	485	14.9	544	2	A41426	cholinesterase (EC
93	484	14.8	544	2	F41426	cholinesterase (EC
94	482	14.8	544	2	B41426	cholinesterase (EC
95	482	14.8	544	2	S41094	cholinesterase (EC
96	481	14.8	544	2	H41426	cholinesterase (EC
97	481	14.8	563	1	PN0493	cholinesterase (EC
98	479	14.7	544	2	S41095	cholinesterase (EC
99	478.5	14.7	544	2	B34089	cholinesterase (EC
100	478	14.7	544	2	E41426	cholinesterase (EC

ALIGNMENTS

RESULT 1

ACHD

cholinesterase (EC 3.1.1.8) precursor [validated] - human

N:Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: A33769; A34683; A34687; A34688; A00772

R:Arpaagau, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.

Biochemistry 29, 124-131, 1990

A:Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co

A:Reference number: A33769; MUID:90212557; PMID:2322535

A:Accession: A33769

A:Molecule type: DNA

A:Residues: 'MSVSNLQGAAGAACISPKYMIPTPKLCHLCRESEIN', 1-602 <ARP>

A:Cross-references: UNIPROT:P06276; GB:M2391; GB:J02879

A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra

R:Prody, C.A.; Zevin-Sonkin, D.; Ghatt, A.; Goldberg, O.; Soreq, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987

A:Title: Isolation and characterization of full-length cDNA clones coding for cholineste

A:Reference number: A26613; MUID:87231856; PMID:3035536

A:Accession: A26613

A:Molecule type: mRNA

A:Residues: 1-133; 'D', 135-602 <PRO>

R:McLennan, C.; Adkins, S.; Chaconnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose

Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987

A:Title: Brain cDNA clone for human cholinesterase.

A:Reference number: A33887; MUID:88016155; PMID:3477799

A:Accession: A33887

A:Molecule type: mRNA

A:Residues: 'MSVSNLQGAAGAACISPKYMIPTPKLCHLCRESEIN', 1-602 <MCT>

A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra

R:Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpaagau, M.; Van der Spek,

Am. J. Hum. Genet. 46, 934-942, 1990

A:Title: Identification of a frameshift mutation responsible for the silent phenotype of

A:Reference number: A34668; MUID:90252779; PMID:2339692

A:Accession: A34668

A:Molecule type: DNA

A:Residues: 143-145; 'VSNNNIIFTCL', <NOG>

A:Note: frameshift mutant in codon for residue 145 (Gly)

R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.

J. Biol. Chem. 262, 549-557, 1987

A:Title: Complete amino acid sequence of human serum cholinesterase.

A:Reference number: A00772; MUID:87109144; PMID:3542989

A:Accession: A00772

A:Molecule type: protein

A:Residues: 29-602 <LOC>

A:Experimental source: plasma

C:Comment: Cholinesterase is present in most cells (except erythrocytes).

C:Genetics:

A:Gene: GDB:BCHB, CHE1

A:Cross-references: GDB:120558; OMIM:177400

A:Map position: 3q26.1-3q26.2

A:Introns: 506/2; 562/1

C:Function:

A:Description: hydrolyzes acylcholines to choline and a carboxylic acid

A:Note: this cholinesterase is highly reactive with organophosphate esters

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein; homocetramer

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-602/Product: cholinesterase #status experimental <MAT>

F:56-556/Domain: cholinesterase homology <CHE>

F:45/85;134,269,284,369,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status

F:226/Active site: Ser #status experimental

Query Match 99.4%; Score 3239; DB 1; Length 602;

Best local similarity 99.7%; Pred. No. 8.5e-240;

Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MDSKVTITICRFLFWILLCLIGKSHTEDDIIATKNGKVGMLTVFGVTAFLGIP 60

Db 1 MDSKVTITICRFLFWILLCLIGKSHTEDDIIATKNGKVGMLTVFGVTAFLGIP 60

QY 61 YAOPLGLRFRKQOSLTKSDINNAKRYANSCCONIDQSPFGHSEMMNPDTLSEDC 120

Db 61 YAOPLGLRFRKQOSLTKSDINNAKRYANSCCONIDQSPFGHSEMMNPDTLSEDC 120

QY 121 LYANWIPAPKPNATVLIWVGGFQGTSSLHVYDGKFLARVRYIVSMNRYVALG 180

Db 121 LYANWIPAPKPNATVLIWVGGFQGTSSLHVYDGKFLARVRYIVSMNRYVALG 180

QY 181 FLALPQNPAPQNGMLPFOQALQWQKNTAFEGNRSYTLFESAGASVSLHLSPG 240

Db 181 FLALPQNPAPQNGMLPFOQALQWQKNTAFEGNRSYTLFESAGASVSLHLSPG 240

QY 241 SHSLFTRAILLOSQSNAPWATSLYEARNRTLNALTKGCRENETEIIKCLRNKDPQEI 300

Db 241 SHSLFTRAILLOSQSNAPWATSLYEARNRTLNALTKGCRENETEIIKCLRNKDPQEI 300

QY 301 LLINEAFVVPYGTPLSVNGPPTVDGDLTMDPDLLELQFKKTOILVGNKDEGTWFLVY 360

Db 301 LLINEAFVVPYGTPLSVNGPPTVDGDLTMDPDLLELQFKKTOILVGNKDEGTWFLVY 360

QY 361 GAPGSKNNSTITTKERQEGKTFPPGVSRGKESILFHTTMDWDORPENYREALGDV 420

Db 361 GAPGSKNNSTITTKERQEGKTFPPGVSRGKESILFHTTMDWDORPENYREALGDV 420

QY 421 VGDYVNICPALFTFKFSQWGNNAFFYFEHRSSKLPWPEWGVHGYIEFVGLPIER 480

Db 421 VGDYVNICPALFTFKFSQWGNNAFFYFEHRSSKLPWPEWGVHGYIEFVGLPIER 480

QY 481 RDNVTKAEILSRSLYKMANPAKGNPNTONSTSPVPESTOKYLLTNTSESTRIMT 540

Db 481 RDNVTKAEILSRSLYKMANPAKGNPNTONSTSPVPESTOKYLLTNTSESTRIMT 540

QY 541 KLRAGQCRWTSFPFVLEMTGNIDEAEWEMKAGHRNNYMMWMDKQNFNDYTSKESCV 600

Db 541 KLRAGQCRWTSFPFVLEMTGNIDEAEWEMKAGHRNNYMMWMDKQNFNDYTSKESCV 600

QY 601 GL 602

Db 601 GL 602

RESULT 2

C39768

cholinesterase (EC 3.1.1.8) - rabbit

N:Alternate names: butyrylcholinesterase

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S10255; C39768

R:Jbilo, O.; Chaconnet, A.

Nucleic Acids Res. 18, 3990, 1990

A:Title: Complete sequence of rabbit butyrylcholinesterase.

A:Reference number: S10255; MUID:90326526; PMID:2374720

A:Accession: S10255

A:Molecule type: translation not shown

A:Status: translation not shown

A:Residues: 1-581 <DBI>

A:Cross-references: UNIPROT:P21927; EMBL:X52090; NID:g1476; PIDN:CAA3308.1; PID:g137027;

R:Arpaagau, M.; Chaconnet, A.; Maesson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogr

J. Biol. Chem. 266, 6966-6974, 1991

A:Title: Use of the phosphoryl chain reaction for homology probing of butyrylcholinester

A:Reference number: A39768; MUID:91201348; PMID:2016308

A:Accession: C39768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 75-215 <ARP>

A:Cross-references: GB:M62779; NID:g164788; PIDN:AAA3169.1; PID:g164789

C:Genetics:

A:Introns: 485/2; 541/1

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein

F:35-535/Domain: cholinesterase homology <CHE>

Query Match 87.6%; Score 2855.5; DB 2; Length 581;
 Best Local Similarity 91.4%; Pred. No. 1.8e-210;
 Matches 531; Conservative 12; Mismatches 37; Indels 1; Gaps 1;

QY 21 MLIGKSTHEDDIIITATKNGKRGKMLVFGSTVTAFLGIPPAQPLRLRKRKQSLTKW 80
 DB 1 MVRSSSHTE-DVITITTKNGRIRGINLPVFGGTVAFLGIPPAQPLRLRKRKQSLTKW 59
 QY 81 SDIWMARKYANSCCONIDOSFPGHSGEMNPNNTDLSBDCLYLWVWIPAPKKAATVLIW 140
 DB 60 SDIWMARKYANSCCONIDOSFPGHSGEMNPNNTDLSBDCLYLWVWIPAPKKAATVLIW 119
 QY 141 IYGGFPGTGTSSLHYDGKFLARVERVIVSMNRYVAGLGLALPGNPEAPGNMGLPQQ 200
 DB 120 IYGGFPGTGTSSLHYDGKFLARVERVIVSMNRYVAGLGLALPGNPEAPGNMGLPQQ 179
 QY 201 LALQWVQKNTAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILLOSGFAPMA 260
 DB 180 LALQWVQKNTAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILLOSGFAPMA 239
 QY 261 VTSLYEARNRTLNKLTCGSRNEMTEIICKLRKNDPOEILNEAFVVPYGTPLSVNPGP 320
 DB 240 VMSIHERNRTLTAKTVGSGTENETETICKLRKNDPOEILNEAFVVPYGTPLSVNPGP 299
 QY 321 TVDGDPLTMDPDLLELGQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSITTRKSFQ 380
 DB 300 TVDGDPLTMDPDLLELGQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSITTRKSFQ 359
 QY 381 GLKIFPGVGFPGESLIFHYTWDVDDORPENRYBALGDVVDNFCPLAEFTKSEW 440
 DB 360 GLKIFPGVGFPGESLIFHYTWDVDDORPENRYBALGDVVDNFCPLAEFTKSEW 419
 QY 441 GNNAFYFFFEHRSKLLPMPWGMVGHGEIEFVGLPLERNDYTKABEILSRISIVRMA 500
 DB 420 GNNAFYFFFEHRSKLLPMPWGMVGHGEIEFVGLPLERNDYTKABEILSRISIVRMA 479
 QY 501 NFAKGNPNETONNSTSWPVFKSTEOKYTLTNTSESTRIMTKLRAQOQCFWTSFPPKYLEM 560
 DB 480 NFAKGNPNETONNSTSWPVFKSTEOKYTLTNTSESTRIMTKLRAQOQCFWTSFPPKYLEM 539
 QY 561 TGNIDAEWEWKAGFHRNNYMDWKQFNDYTSKESCVGL 601
 DB 540 TGNIDAEWEWKAGFHRNNYMDWKQFNDYTSKESCVGL 580

RESULT 3

S70849
 Cholinesterase (EC 3.1.1.8) - mouse
 N:Alternate names: butyrylcholine esterase
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence revision 08-Nov-1996 #text_change 09-Jul-2004
 A:Accession: S70849; S15680; A39768
 R:Taylor, P.
 submitted to the EMBL Data Library, August 1992
 A:Reference number: S70849
 A:Accession: S70849
 A:Molecule type: nucleic acid
 A:Residues: 1-603 <TRY>
 A:Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:G191579; PIDN:AAA37328.1; PID:G1915
 R:Schumacher, T.L.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
 Neuron 5, 317-327, 1990
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
 A:Reference number: JH0314; MUID:90380423; PMID:2400605
 A:Accession: S15680
 A:Status: nucleic acid sequence not shown
 A:Molecule type: nucleic acid
 A:Residues: 30-128, 'P', 130-603 <RAC>
 A:Cross-references: EMBL:M99492
 R:Apagau, M.; Chalmers, A.; Mason, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
 J. Biol. Chem. 266, 6966-6974, 1991
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
 A:Reference number: A39768; MUID:91201348; PMID:2016308

A:Accession: A39768
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 97-128, 'P', 130-237 <ARP>
 C:Superfamily: cholinesterase; cholinesterase; cholinesterase; glycoprotein
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:57-557/Domain: cholinesterase homology <CH>

Query Match 79.5%; Score 2593; DB 2; Length 603;
 Best Local Similarity 80.4%; Pred. No. 2.4e-190;
 Matches 475; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

QY 12 FLWFLLCMLIGKSTHEDDIIITATKNGKRGKMLVFGSTVTAFLGIPPAQPLRLR 71
 DB 13 FLWILLCLMPFGKSHTEEDFIITTKGRVGLSMPLGCTVTAFLGIPPAQPLRLR 72
 QY 72 KKQSLTKMSDINNAATYANSCCONIDOSFPGHSGEMNPNNTDLSBDCLYLWVWIPAPK 131
 DB 73 KKQSLTKMSDINNAATYANSCCONIDOSFPGHSGEMNPNNTDLSBDCLYLWVWIPAPK 132
 QY 132 PKNATVLIWVYGGFPGTGTSSLHYDGKFLARVERVIVSMNRYVAGLGLALPGNPEAP 191
 DB 133 PKNATVLIWVYGGFPGTGTSSLHYDGKFLARVERVIVSMNRYVAGLGLALPGNPEAP 192
 QY 192 GNNGLPQQLALQWVQKNTAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILQ 251
 DB 193 GNNGLPQQLALQWVQKNTAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILR 252
 QY 252 SGSPNAPWATSLYEARNRTLNKLTCGSRNEMTEIICKLRKNDPOEILNEAFVVPY 311
 DB 253 SGSPNAPWATSLYEARNRTLNKLTCGSRNEMTEIICKLRKNDPOEILNEAFVVPY 312
 QY 312 TPISVNFPGTVDDPLTMDPDLLELGQFKKTOILVGNKDEGTWFLVYGAPGSKDNNS 371
 DB 313 TPISVNFPGTVDDPLTMDPDLLELGQFKKTOILVGNKDEGTWFLVYGAPGSKDNNS 372
 QY 372 IITRKEFQGLKIFPGVGFPGESLIFHYTWDVDDORPENRYBALGDVVDNFCPLAE 431
 DB 373 IITRKEFQGLKIFPGVGFPGESLIFHYTWDVDDORPENRYBALGDVVDNFCPLAE 432
 QY 432 EPTKPSSEMNNAPFYFFFEHRSKLLPMPWGMVGHGEIEFVGLPLERNDYTKABEIL 491
 DB 433 EPTKPSSEMNNAPFYFFFEHRSKLLPMPWGMVGHGEIEFVGLPLERNDYTKABEIL 492
 QY 492 SRSIVKMANFAKGNPNETONNSTSWPVFKSTEOKYTLTNTSESTRIMTKLRAQOQCFW 551
 DB 493 SRSIVKMANFAKGNPNETONNSTSWPVFKSTEOKYTLTNTSESTRIMTKLRAQOQCFW 552
 QY 552 SFPKYLEMTGNIDAEWEWKAGFHRNNYMDWKQFNDYTSKESCVGL 602
 DB 553 SFPKYLEMTGNIDAEWEWKAGFHRNNYMDWKQFNDYTSKESCVGL 603

RESULT 4

ACRYE
 acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric ray
 N:Alternate names: acetylcholinesterase, asymmetric form
 C:Species: Torpedo californica (Pacific electric ray)
 C:Date: 17-Mar-1987 #sequence revision 08-Nov-1996 #text_change 09-Jul-2004
 A:Accession: A00773; A60820; A31962; A23902; B4117; S15677
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphree-Guigley, K.; Taylor, S.S.; Fr
 Nature 319, 407-409, 1986
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its c
 A:Reference number: A00773; MUID:86118676; PMID:3753747
 A:Accession: A00773
 A:Molecule type: mRNA
 A:Residues: 'NS', 11-596 <SCH>
 A:Cross-references: UNIPROT:P04058; GB:X03439; NID:964389
 A:Experimental source: electric organ
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature prote
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphree-Guigley, K.; Taylor, S.S.; Fr
 Fed. Proc. 45, 2376-2381, 1986
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and functi

A:Reference number: A60820; MUID:87054662; PMID:3536598
 A:Accession: A60820
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 22-596 <SC2>
 R:Schumacher, M.; Mauler, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase
 A:Reference number: A92701; MUID:89066695; PMID:3198606
 A:Accession: A31962
 A:Molecule type: mRNA
 A:Residues: 1-23 <SC3>
 A:Cross-references: EMBL:X03439; NID:964389
 A:Experimental source: clones AChE-11 and AChE-18
 A:Note: revision to sequence A00773
 A:Accession: B31962
 A:Molecule type: DNA, mRNA
 A:Residues: 499-565 <SC4>
 A:Cross-references: GB:X03439; NID:964389
 A:Experimental source: Clone AChE-1
 R:MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase
 A:Reference number: A23902; MUID:86008285; PMID:3900071
 A:Accession: A23902
 A:Molecule type: protein
 A:Residues: 22, 'B', 24-45, 214-237 <MAC>
 A:Note: active site Ser identification
 R:Kreienkamp, H.D.; Weise, C.; Raba, R.; Aayiksear, A.; Huch, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo
 A:Reference number: A41117; MUID:91296772; PMID:2068091
 A:Accession: B41117
 A:Molecule type: protein
 A:Residues: 100-108 <KRE>
 A:Note: substrate binding site
 R:Mauler, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A:Title: Single gene encodes glycoprophospholipid-anchored and asymmetric acetylcholinesterase
 A:Reference number: F50113; MUID:90166618; PMID:2306366
 A:Accession: S15677
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 557-596 <MAU>
 A:Cross-references: EMBL:X56516
 R:MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.
 A:Reference number: A43099; MUID:87008586; PMID:3759980
 A:Contents: annotation; disulfide bonds
 R:Susman, J.L.; Harel, M.; Silman, I.
 submitted to the Brookhaven Protein Data Bank, October 1991
 A:Reference number: A50061; PDB:1ACE
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of R:Susman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.
 Science 253, 872-879, 1991
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic AChE
 A:Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of R:Susman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.
 C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a holoesterase occurs on the outer surfaces of cell membranes, including those of erythrocytes
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of C:Function:
 A:Description: hydrolyzes acetylcholine to choline and acetate
 A:Pathway: neurotransmitter degradation
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein
 F:1-21/DNA: signal sequence #status predicted <SIG>
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
 F:51-551/DNA: cholinesterase homology <CHS>
 F:80-478, 554/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:88-115, 275-286, 423-542/Disulfide bonds: #status experimental
 F:105/Binding site: substrate (Trp) #status experimental

F:221/Active site: Ser #status experimental
 F:348, 461/Active site: Glu, His #status predicted
 F:437/Binding site: carbohydrate (asn) (covalent) #status experimental
 F:593/Disulfide bonds: interchain #status experimental

Query Match 55.0%; Score 1791.5; DB 1; Length 596;
 Best Local Similarity 53.2%; Pred. No. 5, 1e-129;
 Matches 314; Conservative 111; Mismatches 160; Indels 5; Gaps 3;

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QY 13 LWFLLICMLICKSTHEDIIITATKNGVKGNNLTVFGSTVAFPGIPAPQPLRLRPK 72
DB 12 LHLVVLCO--ADDSSE--LVNTKSGKMGKRVPLSHISAFICIPAEPPVGMKFR 67
QY 73 KPSQSLTKMSDINWATKRYANCCONIDQSPGFHGGSEMMNPNTDLSBDCILYVWVIAPEK 132
DB 68 RPEPKPKMGVGNWASSTYPPNCCQYDEQPGFSGSEMMNPNNEMSEDCILYVWVSPRP 127
QY 133 KNATVLIWYGGGPGTGTSSLSHYDGKFLARVERIVVSMYRVGALGFLALPGNPEAG 192
DB 128 KSTYVWVWYGGGFGYSGSSTLDVYNGKYLYAEVYVLSYRVGAFGLALHGSQEAEG 187
QY 193 NMGILPDQCALQWQKNTIAPFGNPKSVTLFGESAGASVSLHLSPGSHLFTRAILQS 252
DB 188 NMGILLDQRAALQWHDNTQFPGSDPKTYTFESAGASVGMHLSPGSRDLFRRAILQS 247
QY 253 GSFNAPWATSLYEARNFTLANLAKLTGCSRENETELIKLRNKDQDELINAEFVVPYGT 312
DB 248 GSNPCMCWASVVAEGRRVAVELGRNMLNGLNDELHCLREKKQDELIDVEMVLPFDS 307
QY 313 PLVNFEGPTVDGDLTMDPDLIELGQFFKTOILVGNKDEGTFLVYGAPEPSKDNNSI 372
DB 308 IFRFSVFPVYIDGFFPPTSLESMNSGNFKTKOILLVGNVDEBSFPLLYGAPPEPSKDSK 367
QY 373 ITRKEFGELKTFEPVSEFGKSLIFHTDWDVDRPENYBEALGDVVGYNFICPALE 432
DB 368 ISKEDMSGVKLSVPRANDGLDAVTLQYTDWDDNNGIKRDKGLDDIDYDNHVICPLMH 427
QY 433 FTKKPESEWGNNAFFYFEHRSKLPWPEWGWGHEIEFVGLPLERDNTYKAEILIS 492
DB 428 FVVKYKTFNGCYLYLFENFRASNLVPEWVGVIHGEIEFVGLPLVKELANTAEBSALS 487
QY 493 RSTVKEMANFAKGNENETQNNSTSPVKSSTEQKTLTINTESTRTMTLRQOQCFFWS 552
DB 488 RRIIMHWATFPAKGNENEPHOSKWPPLTTKEOKTIDINTBPKHQSLRFQVCFWNO 547
QY 553 FPEKVLMTGNIDAEWEMWAGFHRNNYMMDMKQNFNYTSKESCVGL 602
DB 548 FLEKLNATETTDIAERQMKTEFRHNSYIMHMKQNFQHY--SRHESCAEL 596

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RESULT 5

A38868
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
 C:Species: Torpedo marmorata (marbled electric ray)
 C:Date: 23-Apr-1993 #sequence, revision 15-Nov-1996 #ext_change 09-Jul-2004
 C:Accession: A38868; A29682; S15696; A25650
 R:Massoulié, J.; Bon, S.
 submitted to the EMBL Data Library, June 1992
 A:Reference number: A38868
 A:Accession: A38868
 A:Molecule type: mRNA
 A:Residues: 1-599 <MAS>
 A:Cross-references: UNIPROT:P07692; EMBL:X05497; NID:964414; PIDN:CA29047.1; PID:964415
 R:Skorav, J.L.; Krejci, E.; Massoulié, J.
 EMBO J. 6, 1865-1873, 1987
 A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of
 A:Reference number: A29682; MUID:88004392; PMID:2820709
 A:Accession: A29682
 A:Molecule type: mRNA
 A:Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>
 A:Cross-references: EMBL:X05497
 R:Skorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;
 EMBO J. 7, 2983-2993, 1988

A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo electric organ
A:Reference number: S01293; PMID:89030590; PMID:3181125
A:Accession: S15696
A:Molecule type: mRNA
A:Residues: 526-599 <S12>
A:Cross-references: EMBL:X13172, NID:964416; PIDN:CAA31570.1; PID:964417
A:Experimental source: clone pACH2
R:Born, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-soluble cholinesterase.
A:Reference number: A91370; PMID:87080761; PMID:3792544
A:Accession: A25650
A:Molecule type: Protein
A:Residues: 25-40, 'G', 42-47 <BON>
C:Genetics:
A:Gene: AChE
C:Function:
A:Description: hydrolyzes acetylcholine to choline and acetate
A:Pathway: neurotransmitter degradation
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein, neurotransmitter
F:1-34/Domain: signal sequence #status predicted <Sig>
F:25-599/Product: acetylcholinesterase #status predicted <MAT>
F:54-554/Domain: cholinesterase homology <CHR>
F:83, 440, 481, 557/Binding site: carbohydate (Asn) (covalent) #status predicted
F:91-118, 278-289, 426-545/Disulfide bonds: #status predicted
F:224, 351, 464/Active site: Ser, Glu, His #status predicted
F:596/Disulfide bonds: Interchain #status predicted

[illegible]

RESULT 6
A39256
acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
C|Species: Homo sapiens (man)
C|Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C|Accession: A39256; S03959
R|Source: H.; Ben-Aiziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw
Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
A|Title: Molecular cloning and construction of the coding region for human acetylcholine-
A|Reference number: A39256; MUID:91088577; PMID:2263619
A|Accession: A39256
A|Molecule type: mRNA; DNA
A|Residues: 1-614 <SR>
A|Cross-references: UNIPROT:P22303; GB:M55040; NID:G177974; PIDN:AAA68151.1; PID:G177975
A|Note: this sequence represents composite of clones including clone ABGACHE from adult b
nce should represent an authentic brain splice form
R|Chhajani, V.; Derr, D.; Barles, B.; Schnell, E.; August, T.
FEBS Lett. 247, 279-282, 1989
A|Title: Purification and partial amino acid sequence analysis of human erythrocyte acety
A|Reference number: S03959; MUID:89232136; PMID:2714437
A|Accession: S03959
A|Molecule type: protein
A|Residues: 256-266, 'Y', 268-273, 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-326, 'Y', 332-351 <CH>
A|Experimental source: erythrocytes
A|Note: this form was a disulfide-linked homodimer
C|Genetics:
A|Gene: GDB:ACHB; YT
A|Cross-references: GDB:118746; OMIM:100740
A|Map position: 7q22-7q22
C|Superfamily: cholinesterase; cholinesterase homology
C|Keywords: alternative splicing; carboxyl ester hydrolase; glycoprotein; phosphatidylch
P-63-569/Domain: cholinesterase homology <CH>

Query Match	52.1%;	Score 1698.5;	DB 2;	Length 614;
Best Local Similarity	52.3%;	Pred. No. 76-122;		
Matches	312;	Conservative 106;	Mismatches 167;	Indels 11; Gaps 6;
Qy	17	LLLCML---IGKSHED--DIIFATKNGKVRGNMLTFVFGSTVTAFLGIPIYAQPELRGRFK	72	
Db	20	LLIMLLGGVGAEGEDAEHLVTVAGRLRGIRLKTGGPVPVSAFLGIPIRAEPPMGRRRL	79	
Qy	73	KPQSLTKMSDIWNAITKYANSCCQNDI0SEPPGFHSGEMMNPTDLSDCILYAWIIPAKP	132	
Db	80	PPEPQPPSGVVDATTFQSVCYQYVDTLYPGEGTEMMNPNNELSSDCILYAWITPYPRP	139	
Qy	133	KNAT-VLIWYIGGGFQGTGSSLHVTYDGKFLAVERVYIVSNYRVGALGFLAPGNPEAR	191	
Db	140	TSPTFVLWVIYGGGFGYSGASSLDVYDGRFLVQAEKRTVLVSNMYRVGAFGLALPGSREAR	199	
Qy	192	GNMGLFDQQLLQWQKNIILARFGNPKSVTLREGSAGASVSLHLILSPGSHSLFTALIQ	251	
Db	200	GNVGLLDRLRLQWQGVNVAARFGDPTSVTLFGSSAGASVGMHLLSPSRGIFHRAVLQ	259	
Qy	252	SGSFNAPAAVTSLYEARNRTNLAKLTGC---SRENETETIKCLANKPOBILINAEAFV	307	
Db	260	SGAPNGPAIYVGMGEARRRATQLAHLVGCPCPGCTGNDTELVACLTTPRAQVLVNHENAV	319	
Qy	308	VPYGTPLSVNGFPTVDGDFLTMDPILLELGOFKKTQILVGNKDEGTWFLVYGABGFSK	367	
Db	320	LPGSVVPFSPFVVPVDDGDFLSDTPREALINAGDFHGLQVLVGVVKBGSGFLVYGABGFSK	379	
Qy	368	DNNSITTRKEFOEGKLTFFPGVSEFGKESILFHYTDVDDQRPENTRYBALGVVDGYNFI	427	
Db	380	DNESIISRAEFLAGVRVGVPOVSDLAABAVALVHYTDMILHPEDPARLREALSDVAGDHNVV	439	
Qy	428	CPALBFTKPSBEMGNNAFFYYFEHSSKLPMBEMNGWNGHGVIEIFPGILPLBRDNYTKA	487	
Db	440	CPVAQGLARLAAQAGRVAYAVFEHRASLTLSWLMNGVPHGVIEIFPGILPLDPSRNYTAE	499	
Qy	488	BEIISRGSIVRKWANFAKYNPEITON-NTSWPVRKSTEQKLTTLNTSTESIRINTKLRQAQ	546	

Db 500 EKIFPAQKLMRYMANFARTGDPNEDPKAPQMPYTAQOQYVSLDRPLEVRKGFJAOA 559
Qy 547 CRFWTSFPPKVLIENTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCVGL 602
Db 560 CAFWNRFLPKLSATDTLDEAEKQWKAEPHRSYVHWKQFNDYTSKESCVGL 614

RESULT 7

JH0811

acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C/Accession: JH0811

R/legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.

J. Neurochem. 60, 337-346, 1993

A/Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul

A/Reference number: JH0811, MUID:93107932, PMID:8417155

A/Accession: JH0811

A/Molecule type: mRNA

A/Residues: 1-614 <LEG>

A/Cross-references: UNIPROT:P37136; GB:S50879; NID:g262092; PIDN:AA024586.1; PID:g262093

A/Experimental source: stratum

C/Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy

C/Superfamily: cholinesterase; cholinesterase homology

C/Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n

F/1-31/Domain: signal sequence #status predicted <SIG>

F/32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>

F/63-569/Domain: cholinesterase homology <CH>

F/100-127,288-303,440-560/Disulfide bonds: #status predicted

F/234,365,478/Active site: Ser, Glu, His #status predicted

F/296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 1693.5; DB 2; Length 614;

Best Local Similarity 52.8%; Pred. No. 1.7e-121;

Matches 315; Conservative 103; Mismatches 168; Indels 11; Gaps 5;

Qy 16 FLILCMILIGKSHTE---DDIIATKXGKRGKMLTVFGGVTAFGLIPYAOPPLGLRLF 71
Db 19 FLILSLGCGARAGREDPOLVVRGQRLGRLKAPGVSAFLGIPRAEPVGSRRF 78
Qy 72 KKPSQLTKMSDINATKYANSCCONIDQSPFGHSEMMNNTDLSBDCIYLVNIPAK 131
Db 79 MPPEPKPMGSDILDTATFQNVCYQYVDLTPGFEGETEMNNPNEISBDCIYLVNIPAK 138
Qy 132 PKNAT-VLIWYGGGFGTGTSSLVHYDQKFLARVERIVVSMYRVGALGFLALPGNPEA 190
Db 139 PTSEPTPLIWIYGGGFYSGASLSDVYDGRFLAQVEGAVLVSMYRVGTFGLALPGSREA 198
Qy 191 PGNNGLPDQOLALQWOKNIAAFGPNKSVTLFGESAGASVSLHLSPGSHSLFTRAIL 250
Db 199 PGNVGLDQRLALQWOKNIAAFGSDPMSTVTLFGESAGASVGMHILSLPERSLFRHAYL 258
Qy 251 QSGSFNPMWAVTSLYEARNRTLNIAKLTCG---SRENETEIIKCLRNKPOEILLNEAF 306
Db 259 QSGFPGNPMWAVTSLYEARNRTLNIAKLTCG---SRENETEIIKCLRNKPOEILLNEAF 318
Qy 307 VVPYGTPLSVNFGTVDGFLITMPDILLEGOKTQIILVGNKDEGTWLVYGAAGFS 366
Db 319 VLPQESIFRFSEFVVDGFLSDPDDALINTGDFODQVILVGVKDEGSYFLVYGVGFS 378
Qy 367 KDNNSITTRKKEFGQGLKIFPPGVSEFGKESILPHYTWDVDDQRENTREALGDVVGYNF 426
Db 379 KDNNSITTRKKEFGQGLKIFPPGVSEFGKESILPHYTWDVDDQRENTREALGDVVGYNF 438
Qy 427 ICPALFTKFSSEWGNNAFFYFPEHRSKLPWPMGMGMGYEIEFVFGGLPLERRDNYTK 486
Db 439 VCPYLAQLAGRLAAGARVAYVIFPHRASLTLPMLMGVPHGYEIEFIFGLPLDSINVTY 498
Qy 487 ABEILSSIVKMANFAKYNPNETQNN-STSWPFVSTKQKYLTLNTESTRITNTKLRQAQ 545
Db 499 EERIFAQRLMOWNTNFATGDPNDRDSKSPRPMPYTTAAQOQYVSLNKLPLEVRKGFJAOA 559

Qy 546 QCRFWTSFPPKVLIENTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCVGL 602
Db 559 TCAFWRFLPKLSATDTLDEAEKQWKAEPHRSYVHWKQFNDYTSKESCVGL 614

RESULT 8

JH0314

acetylcholinesterase (EC 3.1.1.7) precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C/Accession: JH0314

R/Rechinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.

Neuron 5, 317-327, 1990

A/Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternat

A/Reference number: JH0314, MUID:90380429, PMID:2400605

A/Accession: JH0314

A/Molecule type: mRNA

A/Residues: 1-614 <RAC>

A/Cross-references: UNIPROT:P21836; EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845

A/Experimental source: brain

C/Superfamily: cholinesterase; cholinesterase homology

C/Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n

F/1-31/Domain: signal sequence #status predicted <SIG>

F/32-614/Product: acetylcholinesterase #status predicted <MAT>

F/63-569/Domain: cholinesterase homology <CH>

F/100-127,288-303,440-560/Disulfide bonds: #status predicted

F/234/Active site: Ser #status predicted

F/296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 1692.5; DB 2; Length 614;

Best Local Similarity 52.1%; Pred. No. 2e-121;

Matches 314; Conservative 106; Mismatches 172; Indels 11; Gaps 5;

Qy 10 IREPLFMFLILCMILIGKSHTE---DDIIATKXGKRGKMLTVFGGVTAFGLIPYAOP 65
Db 13 IAPPLFLILSLGCGARAGREDPOLVVRGQRLGRLKAPGVSAFLGIPRAEPVGSRRF 72
Qy 66 IGLRFRKKPSQLTKMSDINATKYANSCCONIDQSPFGHSEMMNNTDLSBDCIYLVN 125
Db 73 VGSRRFPKPMGSDILDTATFQNVCYQYVDLTPGFEGETEMNNPNEISBDCIYLVN 132
Qy 126 WIDAPKPKNAT-VLIWYGGGFGTGTSSLVHYDQKFLARVERIVVSMYRVGALGFLAL 184
Db 133 WTPYPPASPTPLIWIYGGGFYSGASLSDVYDGRFLAQVEGAVLVSMYRVGTFGLAL 192
Qy 185 PGNPEAPGNNGLPDQOLALQWOKNIAAFGPNKSVTLFGESAGASVSLHLSPGSHSL 244
Db 193 PGNPEAPGNNGLPDQOLALQWOKNIAAFGSDPMSTVTLFGESAGASVGMHILSLPERSL 252
Qy 245 FTALILQSGSFNPMWAVTSLYEARNRTLNIAKLTCG---SRENETEIIKCLRNKPOEIL 300
Db 253 FTALILQSGSFNPMWAVTSLYEARNRTLNIAKLTCG---SRENETEIIKCLRNKPOEIL 312
Qy 301 LLINEAFVVPYGTPLSVNFGTVDGFLITMPDILLEGOKTQIILVGNKDEGTWLVYGA 360
Db 313 VLBEMHVLTPQESIFRFSEFVVDGFLSDPDDALINTGDFODQVILVGVKDEGSYFLV 372
Qy 361 GARGFSKDNNSITTRKKEFGQGLKIFPPGVSEFGKESILPHYTWDVDDQRENTREALGD 420
Db 373 GARGFSKDNNSITTRKKEFGQGLKIFPPGVSEFGKESILPHYTWDVDDQRENTREALGD 432
Qy 421 VGVYNYFCPLAFTKFSSEWGNNAFFYFPEHRSKLPWPMGMGMGYEIEFVFGGLPLER 480
Db 433 VGVYNYFCPLAFTKFSSEWGNNAFFYFPEHRSKLPWPMGMGMGYEIEFVFGGLPLER 492
Qy 481 RDNVYKAEBILSSIVKMANFAKYNPNETQNN-STSWPFVSTKQKYLTLNTESTRITNT 539
Db 493 SLNVTTEERIFAQRLMOWNTNFATGDPNDRDSKSPRPMPYTTAAQOQYVSLNKLPLE 552
Qy 540 TKLRAQCRFWTSFPPKVLIENTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKES 559
Db 553 RGLRAQCRFWTSFPPKVLIENTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKES 611

Db 485 RTGDPNDPRPKAPQPPYPAAGQVSLRLRLPGVQASRAQACAFNRFLPKLNATD 544
Qy 563 NIDAEWEMWAKGFHRRNNYMDWKQNFNDYTSKESCVGL 602
Db 545 TLDEARQWKAEPFRMSYVHWKQNPDPHY-SKQDRCSDL 583

RESULT 11

S47639
acetylcholinesterase (EC 3.1.1.7) - chicken
C:Species: Gallus gallus (chicken)
C>Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S47639
R:Kendall, W.R.; Rimer, M.; Gough, N.R.
Biochim. Biophys. Acta 1218, 453-456, 1994
A>Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and
A:Reference number: S47639; MUID:94325359; PMID:8049273
A:Accession: S47639
A:Molecule type: mRNA
A:Residues: 1-767 <RAN>
A:Cross-references: UNIPROT:P36196; EMBL:U03472; NID:9623031; PIDN:AAA60456.1; PID:94241
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 45.0%; Score 1466; DB 2; Length 767;
Best Local Similarity 38.9%; Pred. No. 6e-104;
Matches 298; Conservative 89; Mismatches 197; Indels 182; Gaps 7;

Qy 16 FLTLMLIGKSHTEIDII-----IATNGKVRGNNLV--FGGTVAFLGIPYAP 64
Db 5 FLTLMLLSPSPSAHFAVAPRPREVTTGVRGLLPAGSGSTAAAFGLIPAVP 64
Qy 65 PLGLRLRKPKQSL-TKMSDIWNAKTYANSCCONIDSPFGHSEMMNPNTDLSDEL 123
Db 65 PLGLRLRPPPLPIPTWTGIRDAOSOPACQWDTTFPGQSEMMNPKNESDEL 124
Qy 124 NWMLPAKPKNAATLIMVYGGFQGTGSLHYVYKFLARVERIYVSMYRVAGLFLA 183
Db 125 NWMLQKQDPPEPPLVWVYGGFQGTGSLHYVYKFLARVERIYVSMYRVAGLFLA 184
Qy 184 LPPNPEAPGNMGLPDQOLALQWVQNTAFAFGNPKSVTLFESASGAASVSLHLSPSHS 243
Db 185 LAGHRDAPGNVGLMDQRLAQWVDMNAFAGDPLDILTFESASGAASVGHHLSPSHS 244
Qy 244 LFTAILLOSQSFNAPMAVTSLEYEARNTLNAKLTCGSRNETETIICLRKNDQOELLN 303
Db 245 LFRRAVLQSGSPNGPWATIGAEGRRRAAALGRAVGCPCYGNETELGCLRKEADVLG 304
Qy 304 EAPVVPSTPLSVNPGFTVDDPLTMDPDLLELQGF----- 340
Db 305 EGVNPPQSVRRFAFVAVDDGFVYVDSFDVAL-MGDIYVKGEGHGVGGDGGYGVKGG 363
Qy 341 ----- 340
Db 364 DGVKGVGGYGANGVREGDGDGGYGVKEGLREGYGVKEGVGEGDANAYGARVPRPH 423
Qy 341 ----- 340
Db 424 RDETPPDAYGAKGADAYGAKAAPRPHDETS PDAYGAKMPRPHDEASPDYTGAKMP 483
Qy 341 ----- 340
Db 484 RPHRDETPDAYGAKMPRPHRAGGEVLLGAVRVESEYFLVYGVPEFGDNESLSRE 543
Qy 377 EFOEGIKLFFPGSEFGKESILFHTDWVDDQRPENYREALGDVVDYNTFCPALFTTK 436
Db 544 EFLGVRNGVPATLAEAVVLYHTDLDNPNVKNREALDIDYGDHNVVCPILMAAFQR 603
Qy 437 FSEWGNNAFFYYFEHRSKSLPPEPMGVMGCEIFVFVGLPLERDNTKAEILSRIV 496
Db 604 WAORGKAYAYLFDHRSSTLLMPSWGVPHGEIEFVGLPLEPNNYTRREVELSRIM 663

Qy 497 KEMANFAKYNENETONNNTSWPEFKSTEQKYLTLNTESTRYMTLRAQOCNFWTSFEPK 556
Db 664 KYMGAPARKDNGV-GGPRWPPTPSGQRRAHNAAPLPSGHGLRQICAFWTRFLPK 722
Qy 557 VLEMTGNIDEAEWEMWAKGFHRRNNYMDWKQNFNDYTSKESCVGL 602
Db 723 LNAATGPPEDAEREWRLFEFRMSYMGWRTOFEHY-SRODPCATL 767

RESULT 12

A54413
acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: A54413; J29824
R:Arpaug, M.; Pedon, Y.; Cousin, X.; Chateonnet, A.; Berge, J.B.; Fournier, D.; Toutant, J. Biol. Chem. 269, 9957-9965, 1994
A>Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene encodi
A:Reference number: A54413; MUID:94193691; PMID:8144590
A:Accession: A54413
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-620 <AKP>
A:Cross-references: UNIPROT:P38433; GB:X75331; NID:9475060; PIDN:CAA53080.1; PID:9671831
R:Wu, X.; Le, T.T.
A:Description: The sequence of C. elegans cosmid w09b12.
A:Reference number: Z20693
A/Accession: J29824
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-620 <MUX>
A:Cross-references: EMBL:U58731; PIDN:AA00593.1; GSPDB:GN00028
A:Experimental source: strain Bristol N2; clone w09b12
C:Genetics:
A:Gene: CESP:ace-1
A:Map position: X
A:Initons: 13/3; 59/2; 154/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2
A:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:45-567/Domain: cholinesterase homology <CHE>

Query Match 35.0%; Score 1142; DB 2; Length 620;
Best Local Similarity 41.0%; Pred. No. 2.8e-79;
Matches 243; Conservative 94; Mismatches 213; Indels 42; Gaps 14;

Qy 46 LTVPGGTVAFLGIPPAQPPGLRLRKPKQSLTKMSDINNAKTYANSCCONIDSPFGH 105
Db 35 LSGTGRPLRFRFGIPPAEPVGNLRFRKPKQSPKQPMRIPLNATTPNSCTQSEDYTGDFY 94
Qy 106 GSEMMNPNTDLSDELCLYLNWIPA---PKPKATVLIWYGGFQGTGSLHYVYDKFLA 162
Db 95 GSTMKNANTLSDELCLYLNWYVKGXDPNKKLA-WWVYVGGFMSGTALDYDGRILL 153
Qy 163 RVERIVSNMYRVAGLGLTALPNDPAPGNMGLPDQOLALQWVQNTAFAFGNPKSVTL 222
Db 154 VEENVILVAMNYRVSIFGFLYM-NRPEADGNMGMQOLAMKVVHKNIIDIFGDLRITL 212
Qy 223 FGSAGAAVSLSLSPSHSLFTRAILLQSGSFNAPMAVTSLEYEARNTLNAKLTCGS- 281
Db 213 FGSAGAAVSLSLSPSHSLFTRAILLQSGSFNAPMAVTSLEYEARNTLNAKLTCGS- 281
Qy 282 -----RENETEILICLRKNDQOELLNE-AFVVYGTPLSVNPGFTVDDGFLTMDPIL 336
Db 273 MSLLNPYDILLOCQRAADALARENKMAVYREFG---DEPWVYVDDGFLLENAQTSLK 329
Qy 337 LGQFKTKQLILVGNKDEGTWFLVYVYGVAPGFSKNNNSITTRKEQEGKIFPPGSEFGKES 336
Db 330 QGNFKTKQLLAGSNRDESIYFLTYQLPDIFPVAD-FFTKDFTKDRQLWTGKYDILPRQ 388
Qy 397 IL-----FHYTMDV-DQRPENYREALGVVDYNTFCALFETKFSWGNNAFF 446
Db 389 ILKQQLTLAAVLAHYEPQDLVPTPRDWINMDKGLGDYHFTGCVNEALAHYHGGDTTY 448

447 YYPEHRSSKLPWPEMGMVGHGEIEFVFGGLPL-ERRDNYTKABEILSRIVKMANPAKY 505
449 YYPEHRSSKLPWPEMGMVGHGEIEFVFGGLPL-ERRDNYTKABEILSRIVKMANPAKY 508
506 GNPENONNSTS---WPEVSTBEOKYTLTNTST---RIMTKLRAOQCFWTSFPPKV 557
509 GNPENONNSTS---WPEVSTBEOKYTLTNTST---RIMTKLRAOQCFWTSFPPKV 568
558 LEMTGNIDAEWEKAGFHRW-NNYMMDKMGQFNDY-----TSKESCVG 601
569 MAADVADGDPYLVKQMDKQNEYITDMQYHFOYKRYQTYRQSDSBCG 620

RESULT 13
S66236
acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66236
R/Author: N.; Rocheleau, T.; Moccilin, G.; Lee, H.J.; ffrench-Constant, R.
PEBS loci: 368, 461-465, 1995
A/Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene
A/Reference number: S66236; MUID:95361924; PMID:763199
A/Accession: S66236
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-637 <ANT>
A/Cross-references: UNIPROT:Q9TX11
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase
F/1-28/Domain: signal sequence #status predicted <SIG>
F/29-637/Product: acetylcholinesterase #status predicted <MAT>
F/57-594/Domain: cholinesterase homology <CHR>

Query Match 33.8%; Score 1075.5; DB 2; Length 637;
Best Local Similarity 37.8%; Pred. No. 3.5e-74;
Matches 227; Conservative 95; Mismatches 225; Indels 53; Gaps 8;

3 SKYITICIRFLFWLLCMLIGKSHTEDDIIATKNGKVRGMNLTVCYTALGIPYA 62
4 SAVVRLCCNMISLLCTTVISPVYGIPIRLVVOSSGPIRGRSTMVIGREHVHNGVFA 63
63 QPPLGLRFRPKPQSLTKMSDINATKYANSCCONIDSPFGHSEMMNPVTDSECLY 122
64 KPPDGLRFRPKPQSLTKMSDINATKYANSCCONIDSPFGHSEMMNPVTDSECLY 123
123 LNWIPA-----PKRKATVLIWYGGGFQGTGSLH 154
124 LNIWVPTKRLRHGRGLNFGNNDFQDDDDFQROHOSKGLAMLWIIYGGGFMSGTSLD 183
155 VYDGKFLARERVIYVSMNRYVGLALP---GNBPANMGLFPQOALALOWOKNIA 211
184 VYNAEMLAAGNVIVASMOYRVSFGFFYLA PYLNDADAPNGVGLMDQALALRWLKENAK 243
212 AFGGNPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILOSGSFNAPAVTSLEYARN 271
244 AFGDPLPILITFGESAGSSVSLHLSFVTRGLSRGILGSGTINAKRSHMSAKALSA 303
272 LNTAKLTGCS---RENTEIILKLRNKDPOEILINAEFVVPYGTPLSVNFGPTVDPL 327
304 BALIDDCNCNVTLTKDNPVYMNCMRVNDATKISVQO--WNSYSGILGFPAPITDGVFM 361
328 TDMEDILLELQFKKTOILVGNKDEGTWPLVYG-AQFSGKDNNSITTRKEFOGLKIF 386
362 TAPMTMLREANLEGVILVGSNDBEGYFLLYDIFDYFEADAATSLPRDFLEIMNTIF 421
387 PGVSEFGKESILFHYTDMVDDQREPNYREALGDVVDYFNICPALFETPKFSEMGNA 446
422 SKASEPREALITFYTGESGNDGYNQOQVGRSVGDFHFCIPNERPALGLAEGASVY 481
447 YYPEHRSSKLPWPEMGMVGHGEIEFVFGGLPLERRDNYTKABEILSRIVKMANPAKY 506

482 YYPEHRSSKLPWPEMGMVGHGEIEFVFGGLPL-ERRDNYTKABEILSRIVKMANPAKY 505
507 GNPENONNSTS---WPEVSTBEOKYTLTNTST---RIMTKLRAOQCFWTSFPPKV 557
542 NP---ALEGHWVYTYENNTIYFNAEGE---DDLGEKYGKGPATACAFMNDPLRL 595

RESULT 14
JE0150
acetylcholinesterase (EC 3.1.1.7) - house fly
N/Alternate names: choline esterase I; cholinesterase; true cholinesterase
C/Species: Musca domestica (house fly)
C/Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C/Accession: JE0150
R/Huang, Y.; Qiao, C.L.; Williamson, M.S.; Devonshire, A.L.
Chinese J. Biotechnol. 13, 258-263, 1997
A/Title: Characterization of acetylcholinesterase gene from insecticide-resistant housefly
A/Reference number: JE0150
A/Accession: JE0150
A/Molecule type: mRNA
A/Residues: 1-691 <HUA>
A/Cross-references: UNIPROT:O8MXC4; UNIPROT:O8MXC7; UNIPROT:O8MXC5; UNIPROT:O8MXC8; UNIPROT:O8MXC9
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase
F/81-691/Product: acetylcholinesterase #status predicted <MAT>
F/108-645/Domain: cholinesterase homology <CHR>

Query Match 32.1%; Score 1045; DB 2; Length 691;
Best Local Similarity 38.1%; Pred. No. 8.6e-72;
Matches 230; Conservative 99; Mismatches 218; Indels 56; Gaps 13;

8 ICIIRFLP--WFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVCYTALGIPYA 65
9 IC-RGLPATTIILKRSALTSAMTDHLTVOITSPVARGSVYTOGRVHVFTGIPYAKP 117
66 LGRILFRPKPQSLTKMSDINATKYANSCCONIDSPFGHSEMMNPVTDSECLY 125
118 VDDLRFRPKPQSLTKMSDINATKYANSCCONIDSPFGHSEMMNPVTDSECLY 177
126 WIPA-----PKRKATVLIWYGGGFQGTGSLH 154
178 WAPKARLHRGRGTNGEHSKTDODHLISAPONTNGLPIIWIYGGGFMSGTSLD 237
155 VYDGKFLARERVIYVSMNRYVGLALP---ALPG-NPEAPNGMGLFPQOALALOWOKN 209
238 IYNAELMSAVGNIVIVASFOYRLGAFGLHSPVMPGFEERAPGVNGLMDQALALRWLKEN 297
210 IAAFGNPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILOSGSFNAPAVTSLEYARN 269
298 ARAFGNPKSVTLFGESAGSSVSLHLSFVTRGLSRGILGSGTINAKRSHMSAKALSA 357
270 RTNLAKLTGCSR---ENETIILKLRNKDPOEILINAEFVVPYGTPLSVNFGPTVDG 325
358 IGRALVNDCCNASLLEPENQAVMACROVDATKISVQO--WNSYSGILSVPSAPITDGA 415
326 FLTDMEDILLELQFKKTOILVGNKDEGTWPLVYG-AQFSGKDNNSITTRKEFOGLK 384
416 FLPADPMTLTKTDLSDGYTLIGVNDGEGYFLLYDIFDYFEADAATSLPRDFLEIMNT 475
385 FPGVSEFGKESILFHYTDMVDDQREPNYREALGDVVDYFNICPALFETPKFSEMGNA 444
476 IFKASQAREALITFYTGESGNDGYNQOQVGRSVGDFHFCIPNERPALGLAEGASV 534
445 YYPEHRSSKLPWPEMGMVGHGEIEFVFGGLPLERRDNYTKABEILSRIVKMANPAKY 504
535 YYPEHRSSKLPWPEMGMVGHGEIEFVFGGLPLERRDNYTKABEILSRIVKMANPAKY 504
505 GNPENONNSTS---WPEVSTBEOKYTLTNTST---RIMTKLRAOQCFWTSFPPKV 557
595 GNPENONNSTS---WPEVSTBEOKYTLTNTST---RIMTKLRAOQCFWTSFPPKV 557
561 TGN 563

Db 650 IGS 652

RESULT 15

A25363
acetylcholinesterase (EC 3.1.1.7) precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: C6-Aug-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A25363; A33469
R:Hall, L.M.C.; Spierer, P.
EMBO J. 5, 2949-2954, 1986
A:Title: The *ace* locus of *Drosophila melanogaster*: structural gene for acetylcholinesterase
A:Reference number: A25363; MUID:87080281; PMID:3024971
A:Accession: A25363
A:Molecule type: mRNA
A:Residues: 1-746 <HAL>
A:Cross-references: UNIPROT:P07140
A:Note: the authors translated the codon TGG for residue 18 as Cys and AGA for residue 24
R:Fournier, D.; Karch, F.; Bride, J.M.; Hall, L.M.C.; Berge, J.B.; Spierer, P.
J. Mol. Biol. 210, 15-22, 1989
A:Title: *Drosophila melanogaster* acetylcholinesterase gene structure, evolution and mutation
A:Reference number: A33469; MUID:90064544; PMID:2511327
A:Accession: A33469
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 98-746 <POU>
A:Cross-references: GB:X17572
C:Genetics:
A:Gene: FLYBase: Ace
A:Cross-references: FLYBase: FBgn0000024
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
P:164-704/Domain: cholinesterase homology <CHE>

Query Match 32.0%; Score 1044; DB 2; Length 746;
Best Local Similarity 37.9%; Pred. No. 1,1e-71;
Matches 222; Conservative 100; Mismatches 204; Indels 60; Gaps 12;

QY 30 DIIITATKNGKRGKGNMLTVFGGTVTAPLIGIPAPCPPLRLNFKPKQSLTKWSDIMNATKY 89
DB 138 DRLVIVTSSGPRKGSVTVQGRHVHYTGIPAKPKPVEDILRRKVRPAEPHGVLDATGL 197
QY 90 ANSCQONIDQSPFGFHSSEMNPNITDLSBDCILYNVMTAP----- 130
DB 198 SATCQGERYEPFGSGEIRIMNPNTNVSBDCLYINWMAPAKRLRHGRGANGGEHPNQ 257
QY 131 -----KKKNT---VLIMTYGGFQRTGSLSHVYDQGFLLARVERIVVSMNRY 176
DB 258 ADTDLIHNGNONTNGPLIMIMTYGGFMTGSLTLDIYNADIMAAVGNIVASFQRY 317
QY 177 GAGFLATLPGNP-----EAPGNMGLFDQALALQWQKNIAAFGNGPKSVTLFGESAGAA 230
DB 318 GAFGLHLAPPEMPSEFAEAPAGNVGLMDALAIRMLKQNAHAFGNGPEMTLFGESAGSS 377
QY 231 SVSLHLSGSHSLFRALIQSGSRPAAPAAVSLYEARRRTLNTAKLTGCS-----REN 284
DB 378 SVAAQMSAEVPTGLVYKRGMGQGTMAAPWSHMTSEAAVE--IGKALINDCNASMLKTN 435
QY 285 ETEIILKCLNKPQBOEILNEAFVVPVGTPLSVNFGTVDGFLTMPDILLETGOFKKTQ 344
DB 436 PAHVWCSMSVDAKTISVQO--WNSYSGILSPSAAPTIDGATFLPADPMTIMKTAIDLKQYD 493
QY 345 ILIVGNKDEGTWFLVYG-APGSKDNNSIITTRKEFOGLKITFPQGVSEFGKSLFPHYTD 403
DB 494 ILMGNVRDEGTVFLIYDFIDYFKDQDATALPRDKYLEIMNNIFGKATQAEARAIIFQYTS 553
QY 404 WYDDQSPENVRREALGVNVGDYNNFICPALPFTKFSKSWGNNAFPYFEEHSSSLCPPEWNG 463
DB 554 WEGNPGYQN-QQDQIGAVGDHFTCTPNEYAQLARKGASVHYIYFTHRTISLSINGEMNG 612
QY 464 VMHGYIEFVFGPLERRDNYTKAEELISRSIVKRWANFAKGNPNETQNNSTSPVFKS 523

Db 613 VHGDEIEFFPOGLPNNLSIQYRVERELQKRLSLAVIEPAKGNPAQ---DOEENPNSK 669

QY 524 TEOKYLLTNTSTRTMTKLR---AQCRFWTSFFPKYLEMTGNID 565

Db 670 EDVYYTIFSTDK--TEKLARGPLARCSFMNDYLPKYSMAGTCD 713

RESULT 16

QY 390 acetylcholinesterase (EC 3.1.1.7) 1 - green peach aphid

C:Species: Myzus persicae (green peach aphid)

C:Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003

R:Accession: JCT990

R:Name: Shima, T.; Kozaki, T.; Tomita, T.; Kono, Y.

R:Biochem. Biophys. Res. Commun. 307, 15-22, 2003

A:Title: An amino acid substitution on the second acetylcholinesterase in the pirimicard-

A:Reference number: JCT990; PMID:12849975

A:Accession: JCT990

A:Molecule type: mRNA

A:Residues: 1-664 <NAB>

A:Cross-references: GB:AF287291

A:Experimental source: Pirimicard susceptible strain S14

C:Comment: This enzyme is a target for organophosphate and carbamate insecticides at the

C:Keywords: ACHE; acyl pocket; disulphide bond; insecticide resistance

Query Match 31.9%; Score 1038.5; DB 2; Length 664;

Best Local Similarity 37.9%; Pred. No. 2,6e-71;

Matches 214; Conservative 107; Mismatches 204; Indels 39; Gaps 12;

QY 24 GKSTEDDIIATKNGKVRGMLTVFGYTAFLGIPYAPPLGRKRFKKPQSLTWSDI 63

Db 59 GVDPTDES PAVVVS SGVQGYTKI IANREVRVYTGIPFAKPPGPRFRPVAVDPTGV 118

QY 84 MNATKANSCCQNNIDQSFPGFSGEMKNPTDISECLYLNWVIAPAK-----PKAA--- 135

Db 119 LNAITRLNPTCQERYEYFPGFVSEEMNPTKLSIEDCLYINITYPKKQTRHHSNNAHHA 178

QY 136 --TVLIMVYGGGFQGTSSLHVYDGKFLARVERVIVSNMYRVGALGLAL- PGNDP--- 189

Db 179 KIPPLVMIYGGGWSGSGTSDIDYDGLLATFDVMIASMQYRLGAFSGSLYLTPELPEDSD 238

QY 190 -APGNMGLPDQIALQWVQXIIAIFGNGPKSVTLFGESAGAAVSIIHLSRGSLSLFTBA 248

Db 239 DAPGNGIMQALAIKIKENMAAFGADPETITLFGESAGGSVSVALISPETRGVVRG 298

QY 249 ILOGSGFNAPAVVSLSEARNRRLTLAK--LTGCS-----RSENEYIICKLNKPOBI 300

Db 299 ILOGSVNAPS---YMGERRAVDINKKLDDPCNCTSTLDSNPATMSGMAVDASTI 354

QY 301 LINAFAVVPYGTPLSVNFGPTVDGDLTMDPDIILBLGQFKTQIIVGVNKDEGTWFLVY 360

Db 355 --SKKQNNISGILGFSAPFTVDSVLLPERRDLMLAAVNSDIDILIGSLNAGTFFLY 412

QY 361 G-APGFSKDNNSITTRKEPQEGKLIFFPGVSEKGSILFHYDW---VDDQRPENYRE 415

Db 413 DFVDFPDTSLATLPKKEFVOIVNVIFKDTOLERAIIYQYSGWEKKDDDK--YSNOK 470

QY 416 ALGDVGVGNVTCALBFTKFKSEMGNAAPFYVEHSSSLPMPENMGVHNGEIEFVFG 475

Db 471 QLSDVADYFVFCPTNLFANTVSSRGARVYIFFTHRTDHLMGDMGVLHGDGMQVFG 530

QY 476 LPLERDNYTAAEILSRISIVKRWANFAKYNPNETONNSTSPVFSKQKYLTLNTES 535

Db 531 HPLNMSMYNAREDDLSRIMEATFRSLNGTP---VSDDIDPLVSNPDIYHVMVAE 587

QY 536 TRIMTKLAAQCRFWTSFFPKYLE 559

Db 588 LHVGYGPRAACQFQWNGFFPKIAQ 611

RESULT 17

T37254
acetylcholinesterase (EC 3.1.1.7) 4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37254
R:Giruso, M.; Culetto, E.; Combes, D.; Fedon, Y.; Toulant, J.P.; Arpagaus, M.
FEBS Lett. 424, 279-284, 1998
A:Title: Existence of four acetylcholinesterase genes in the nematodes *Caenorhabditis elegans*
A:Reference number: Z21648; MUID:99196570; PMID:9539167
A:Accession: T37254
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-602 <GB>
A:Cross-references: UNIPROT:O61372; EMBL:AF025379; NID:95091493; PIDN:AACT4017.1; PID:5373
A:Experimental source: strain N2
C:Genetics:
A:Gene: ace-4
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

A:Experimental source: clone Y486A

C:Genetics:

A:Gene: CESP:Y486A.8

A:Introns: 24/3; 58/2; 132/2; 241/2; 461/2; 514/2

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 28.7%; Score 937; DB 2; Length 584;

Best Local Similarity 38.4%; Pred. No. 1,2e-63;

Matches 208; Conservative 93; Mismatches 205; Indels 36; Gaps 16;

```

QY 34 IATKNGKVRGMNLTVFGGTVTAFLGIPYAOPPLGRLFRKKPQSLTKMSDIMNATKYANSC 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 34 VQKRLGTVRGTSBDHGKRVSRFLGVFAFPPIEHRFKKPPARPANNGTISANTLSPAC 93
QY 94 CQNIIDQSPFGHSEMMNPNTDLSDCLYNVMIPAPRKNAATVLIWYGGGFGTGSLL 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 FGGRSDYDPTFGHSEMMNPNTDLSDCLYNVMIPAPRKNAATVLIWYGGGFGTGSLL 152
QY 154 HYYDGKFLARVERIVYSNNRVGALGFLALPGNEAPGNMGLFDQOLALQVQKNIAP 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 LLYDGKELATRGNVIVNINRVGPGYLFL-DHEIDVPGNMGLDQOLALYWRDHFSE 211
QY 214 GGNPKSVTLFGESAGASVSLHLSPGSHLFTRAIIQSGSFNAPMAVTSLYEARNETLN 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 212 GGNPARISLVGESAGASIVAHILAPASGLFQNGIIQSGSLDNKMSDSPRAKOKSTA 271
QY 274 LAKLTGSRNENETIICLNKDPQELINEAFVVPYG---TPLSV---NFGPTVDCD 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 LADLVGNCQTKITDQACLRN-TPAQLLIDINVMVGLNLEFPFAIVSKDNQFPHLDG- 329
QY 326 FLTMDPILLELGQFK-KTQIILVGNKDEGTWFLVYAGPFSKDNNSI---ITRKEFOG 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 -----FIAREGYSTDVNLMFGINHDGNFMNITNLAKEF-DKQSVKGLDRDEPHC 382
QY 382 LKIFPVGSEFGKESILFHYTD--WVDQRPEN-YREALGVGDYVNFICPALETKFS 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 VDTAFVQPELVYRAKAYVSDPKCTDPKKTDFTEQVNMVGDYFFTCDSIWFANHP 442
QY 439 EW-GN--NAFFYVEHRSKLPWEMGMVGHGIEFVGLPLERRD-NYTKAEILSRS 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 KMAQNSNVFVYFDQPSANPMPKWTGVHGEIEYVGVPLHNTAGTYKEMDVSEK 502
QY 495 IYKRWANPAKYGNPNTQ-----NSTSWPVKSTEO-KYLLNTESTRIMTKLRAQCR 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 503 VIDFWTTFANTGVSLKRAVGTQKIKWDRYDGTHTMMNITKGSFRMIQELIKVECD 562
QY 549 FW 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 563 LW 564

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RESULT 20

T42399 acetylcholinesterase (EC 3.1.1.7) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T42399

R:Graus, M.; Culetto, E.; Fedon, Y.; Combes, D.; Toutant, J.P.; Arpagaus, M.

submitted to the EMBL Data Library, June 1999

A:Reference number: Z22157

A:Accession: T42399

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-607 <GRA>

A:Cross-references: UNIPROT:O61459; EMBL:AF039650; PIDN:AAAC14022.2

C:Genetics:

A:Gene: ace-3

A:Map position: 2

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

Query Match 28.5%; Score 930; DB 2; Length 607;

Best Local Similarity 38.2%; Pred. No. 4.5e-63;

Matches 207; Conservative 93; Mismatches 206; Indels 36; Gaps 16;

```

QY 34 IATKNGKVRGMNLTVFGGTVTAFLGIPYAOPPLGRLFRKKPQSLTKMSDIMNATKYANSC 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 34 VQKRLGTVRGTSBDHGKRVSRFLGVFAFPPIEHRFKKPPARPANNGTISANTLSPAC 93
QY 94 CQNIIDQSPFGHSEMMNPNTDLSDCLYNVMIPAPRKNAATVLIWYGGGFGTGSLL 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 FGGRSDYDPTFGHSEMMNPNTDLSDCLYNVMIPAPRKNAATVLIWYGGGFGTGSLL 152
QY 154 HYYDGKFLARVERIVYSNNRVGALGFLALPGNEAPGNMGLFDQOLALQVQKNIAP 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 LLYDGKELATRGNVIVNINRVGPGYLFL-DHEIDVPGNMGLDQOLALYWRDHFSE 211
QY 214 GGNPKSVTLFGESAGASVSLHLSPGSHLFTRAIIQSGSFNAPMAVTSLYEARNETLN 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 212 GGNPARISLVGESAGASIVAHILAPASGLFQNGIIQSGSLDNKMSDSPRAKOKSTA 271
QY 274 LAKLTGSRNENETIICLNKDPQELINEAFVVPYG---TPLSV---NFGPTVDCD 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 LADLVGNCQTKITDQACLRN-TPAQLLIDINVMVGLNLEFPFAIVSKDNQFPHLDG- 329
QY 326 FLTMDPILLELGQFK-KTQIILVGNKDEGTWFLVYAGPFSKDNNSI---ITRKEFOG 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 -----FIAREGYSTDVNLMFGINHDGNFMNITNLAKEF-DKQSVKGLDRDEPHC 382
QY 382 LKIFPVGSEFGKESILFHYTD--WVDQRPEN-YREALGVGDYVNFICPALETKFS 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 VDTAFVQPELVYRAKAYVSDPKCTDPKKTDFTEQVNMVGDYFFTCDSIWFANHP 442
QY 439 EW-GN--NAFFYVEHRSKLPWEMGMVGHGIEFVGLPLERRD-NYTKAEILSRS 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 KMAQNSNVFVYFDQPSANPMPKWTGVHGEIEYVGVPLHNTAGTYKEMDVSEK 502
QY 495 IYKRWANPAKYGNPNTQ-----NSTSWPVKSTEO-KYLLNTESTRIMTKLRAQCR 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 503 VIDFWTTFANTGVSLKRAVGTQKIKWDRYDGTHTMMNITKGSFRMIQELIKVECD 562
QY 549 FW 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 563 LW 564

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RESULT 21

T33842 hypothetical protein Y44E3A.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33842

R:Moessner, J.; Graves, T.; Kepler, D.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z21422

A:Accession: T33842

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-532 <MOE>

A:Cross-references: UNIPROT:O61371; EMBL:AF106589; PIDN:AACT8228.1; GSPDB:GN00019; CESP:Y

A:Experimental source: strain Bristol N2; clone Y44E3A

C:Genetics:

A:Gene: CESP:Y44E3A.2

A:Map position: 1

A:Introns: 16/3; 84/3; 143/2; 219/3; 298/3; 440/2

C:Superfamily: cholinesterase; cholinesterase homology

Query Match 27.4%; Score 893; DB 2; Length 532;

Best Local Similarity 40.8%; Pred. No. 2.5e-60;

Matches 201; Conservative 79; Mismatches 169; Indels 44; Gaps 16;

```

QY 47 TVFGTVTAFLGIPYAOPPLGRLFRKKPQSLTKMSDIMNATKYANSCQNIIDQSPFGH 106
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17 TPDGAKVSAPLGVYAKPPIGSRFRKMAEMIDNWSGELAKTLAKTYLTIDSAFPQFPG 76

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Qy 107 SEMNPTDISEDCLYLVNVI-PAPKPKATVLIYGGGFGTGTSSLHVVDGKLAVER 166
Db 77 AEMNPPGALISEDCLANNIYW--PEDHDGSMWVIYGGGFGTGTSSLDIVSGSYFAKEN 134
Qy 167 VIVSMNVGALGFLPALGNPEAPGNKGLFDQOLALQWOKNIAFGNPKSYTLFGES 226
Db 135 TIIVNVNVRILCPFGFLYFGDDSPIOGNNGMLDDOOLALRWHEINIGAFGGRSRVTLTGEES 194
Qy 227 AGASVSLHLISPGSHSLFTRAILLOSSEFNAPMVAVLSYEARNRNTLMAKTGCSRENET 286
Db 195 AGASSTTAHLPEAPSHKYTEFNIIAKSGSIINSMASATPPTMLDSFLRLAKVNCSSFDPM 254
Qy 287 EIIKLRNKDPOEILLNEAFV--PYGTPLSVNGP--TVDDGFYITDMPDILLLEIG--QFK 341
Db 255 AIVKCLRSV--PAHVQAEADNIGDIPGPMTFAYVPSVDANPF--QODVFOQLANKQFK 311
Qy 342 K-TQILVGNVNDCEGTFLV--GAP--GFS-----KNNNSIIRKKEQDEKLTFEP 387
Db 312 KDVNIIRFSVDEGTWLPYMSLPKYGPAANHITSAEDPHNRLLITRDHSESWRAMPP 371
Qy 388 GVSEFGKESILFHY-----TDVVDQRENYREALGDVGVNFPICPALBETKFESE 439
Db 372 YFA--GSLTVLNAIMNNSYEHVSTSNVPER---YRDGARVLGDLFTGSLIDPADLID 426
Qy 440 --KGNNAFFTYFEHRSSKLPMPENMGVMHGYEIEFVGLPLERKDNITKA---EELISR 493
Db 427 NIFG-NVMYFYFTRSSANPMPKMGVMHGYEIEVAFQGPYWRPHLYDQTHLEDKRLSS 485
Qy 494 SIVKRWANFAKYG 506
Db 486 IIMQIMANFANTG 498

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RESULT 22
A34329
C:60K esterase (EC 3.1.1.-) isoform 2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34329
R:Ozols, J.
J. Biol. Chem. 264, 12533-12545, 1989
A:Title: Isolation, properties, and the complete amino acid sequence of a second form of
A:Reference number: A34329; MUID:89308686; PMID:2745458
A:Accession: A34329
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-532 <OZO>
A:Cross-references: UNIPROT:P14943
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
P:32-517/Domain: cholinesterase homology <CHP>
P:201,430/Active site: Ser, His #status Predicted

```

	Query Match	23.1%	Score 754;	DB 2;	Length 532;
	Best Local Similarity	36.1%;	Pred. No. 1.1e-49;		
	Matches	199;	Conservative	90;	Mismatches 202; Indels 60; Gaps 22;
Qy	36	TKNGKRGKMLTVGG--GTVATFAGIPIYAQPPGLRPRKFKQSTIKRSDIMNATKYNASC		93	
Db	10	THIQVRRSLVHVHGTADGAVHTFLGIPKPKPLGLRPRAPPEPAEBAASGVADGTSIPAMC		69	
Qy	94	QNT----DQSPFGFHGSEMNPNTDLSDDCYLYNWVTP--APRKQNTVLMIWGGGFGQT		148	
Db	70	LQNLAINDDVDVLLHFTP---PSIPMSDDCYLYNIYSPAHARREGSDLPVWYMTWGGGLTM		126	
Qy	149	GTSSLIHYDGFKLARVERVIVVSMNYRVALGFLALPCGNPAEPNMGLFDQQLALQWYK		208	
Db	127	GMAAM--YDGSALAAFEDEVVVVTTQYRGLGVIGFHS--TGDDQATNGHGLDQVALRWQK		183	
Qy	209	NIAAFGNGPKSVTLFGESAGAASVLIHLSPGSSILFRALITLQSGSFPAAPAYALVLEAR		268	
Db	184	NIHFGNGPKGVTLFGESAGGTSVSHVLSPMQGLFPGALIMESIVALLPGLITSSSEVV		243	

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OY 269 NRTLNLAKLTGCSRNNEETIIKCLRKNDQOEIL-LNEAFVVPVGTPLSVNGFPVDDDFL
Db 244 STV--VAHLSRCGQVDSFELVRCIRAKSSEEMALIQVFLLIG-----VDDGFLL 292
OY 338 TDMPDLLELGQFKKTOILGVNKKEGTW---FLVYGAPGFSKDNNSITRKEFQGLK 383
Db 293 PRHPELLALADFGVPSIIGINDBEGMILPRLLALIDPQEBRDQAM--REIMHQATK 350
OY 384 --IFFPGVSEFGKESIIFHYTDMVDDQRENTREALGDVVGDNYPICPALEFTTKKSEWG 441
Db 351 QLMLEPPALGDL---LMDEYMGSNED--PKHILMAQFQEMMADAMFVPALR-VAHLORSH 403
OY 442 NNAAFYYEYEHRS--KLPRPMAGVNHGYEIEVF-----GLPLERRRNYTAEIILS 492
Db 404 APTYYEEFOHRSPFTKDLRPPHVRADHGEVVFVFSHLLGSKVPL-----TDEEILLS 457
OY 493 RSIYERMANFAYGNPNETQNNSTSWPVFKSTQKTLTLNTESTRIMTKLRAOCRFWTS 552
Db 458 RRVMTYMANFAANRPNN--GEGLAHPLF-DLDQRYLLQNMQPA-VGQALKARRLOFWTH 513
OY 553 FFP-KYLEWYG 562
Db 514 TLDPQVQELRG 524

```

RESULT 23
G39768
cholinesterase (EC 3.1.1.8) - rhesus macaque (fragment)
C.Species: Macaca mulatta (rhesus macaque)
C.Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C.Accession: G39768
R.Airgagnas, M.; Chittomet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogi
U. Biol. Chem. 266, 6586-6974, 1991
A.Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase
A.Reference number: A39768; MUID:91201348; PMID:2016308
A.Accession: G39768
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-141 <ARP>
A.Cross-references: UNIPROT:P32751; GB:M62777; NID:G342078; PIDN:AAA36836.1; FID:G342079
C.Superfamily: cholinesterase, cholinesterase homology
C.Keywords: carboxylic ester hydrolase, glycoprotein
F.1-141/Domain: cholinesterase homology (fragment) <CHE>

```

Query Match Similarity 23.1%; Score 753; DB 2; Length 141;
      Best Local Similarity 100.0%; Pred. No. 1.9e-50;
      Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 NIDGFFPGHGEEMNPNTLSEDCLYLNWVIPAPKPKKATVLIMWYGGFQGTSSLAH 155
Db 1 NIDGFFPGHGEEMNPNTLSEDCLYLNWVIPAPKPKKATVLIMWYGGFQGTSSLAH 60

Qy 156 YDGRKLARVERIYVSMNRVAGALGFALPGNPEAGCNKGLFPOQALQWVQKIIAIFGG 215
Db 61 YDGRKLARVERIYVSMNRVAGALGFALPGNPEAGKNGGLFPOQALQWVQKIIAIFGG 120

Qy 216 NPKSVTLFGESAGAASVSLHL 236
Db 121 NPKSVTLFGESAGAASVSLHL 141

RESULT 24
JC5408
carboxylesterase (EC 3.1.1.1) - human
C.Species: Homo sapiens (man)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
JCAccession: JC5408
R.Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A.Title: Molecular cloning and characterization of a novel putative carboxylesterase, pre
A.Reference number: JC5408; MUID:97269502; PMID:9144407
A.Accession: JC5408
A.Molecule type: mRNA

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Thu Jan 6 10:14:55 2005

us-09-748-739a-2.rpr

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Search completed: January 6, 2005, 09:41:42
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:21:17 ; Search time 161 Seconds
(without alignments)
1341.336 Million cell updates/sec

Title: US-09-748-739A-2

Perfect score: 3260
Sequence: 1 MDSKVITICIRFLFWFLIC.....MDWKQFNFDYTSKSCVGL 602Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3260	100.0	602	5	AAOI8897 Human but
2	3239	99.4	602	3	AAV59235 Human but
3	3239	99.4	602	3	AAV49471 Human wil
4	3239	99.4	602	3	AAV44573 Human wil
5	3239	99.4	602	6	ABR62392 Human but
6	3239	99.4	602	7	ADP90908 Human hep
7	3235	99.2	602	3	AAV44574 Human but
8	3234	99.2	602	3	AAV49483 Human but
9	3233	99.2	602	2	AAV37442 Full-Leng
10	3232	99.1	602	3	AAV49474 Human but
11	3232	99.1	602	3	AAV49473 Human but
12	3232	99.1	602	3	AAV49475 Human but
13	3231	99.1	602	3	AAV49472 Human but
14	3231	99.1	602	3	AAV49476 Human but
15	3230	99.0	602	3	AAV49477 Human but
16	3228	99.0	602	3	AAV49484 Human but
17	3228	99.0	602	3	AAV49478 Human but
18	3227	99.0	602	3	AAV49486 Human but
19	3227	99.0	602	3	AAV49485 Human but
20	3227	99.0	602	3	AAV49488 Human but
21	3226	99.0	602	3	AAV49487 Human but
22	3225	98.9	602	3	AAV49482 Human but
23	3224	98.9	602	3	AAV49481 Human but
24	3223	98.9	602	3	AAV49480 Human but
25	3223	98.9	602	3	AAV49479 Human but

26	3110	95.4	574	7	ABW00722 Human but
27	3107	95.3	574	8	ADRO1039 Human but
28	3103	95.2	574	8	ADRO1047 Human but
29	3102	95.2	574	8	ADRO1051 Human but
30	3102	95.2	574	8	ADRO1035 Human but
31	3101	95.1	574	8	ADRO1041 Human but
32	3100	95.1	574	8	ADRO1037 Human but
33	3099	95.1	574	5	AAOI8944 Human but
34	3098	95.0	574	8	ADRO1049 Human but
35	3096	95.0	574	5	AAE25235 Human but
36	3096	95.0	574	5	AAOI8982 Human but
37	3096	95.0	574	5	AAOI8898 Human but
38	3096	95.0	574	6	ABR62391 Human but
39	3096	95.0	574	7	ABW00695 Human but
40	3096	95.0	574	8	ADP44639 Human but
41	3096	95.0	574	8	ADRO1077 Human but
42	3095	94.9	574	8	ADRO1045 Human but
43	3093	94.9	574	8	ADRO1059 Human but
44	3093	94.9	574	8	ADRO1075 Human but
45	3092	94.8	574	5	AAOI8977 Human but
46	3092	94.8	574	7	ABW00723 Human but
47	3092	94.8	574	8	ADRO1080 Human but
48	3091	94.8	574	5	AAOI8979 Human but
49	3091	94.8	574	5	AAOI8960 Human but
50	3090	94.8	574	5	AAOI8983 Human but
51	3090	94.8	574	5	AAOI8945 Human but
52	3090	94.8	574	8	ADP44833 Human but
53	3090	94.8	574	8	ADRO1073 Human but
54	3089	94.8	574	8	ADRO1861 Human but
55	3089	94.8	574	5	AAOI8940 Human but
56	3089	94.8	574	8	ADRO1079 Human but
57	3089	94.8	574	8	ADRO1078 Human but
58	3088	94.7	574	7	ABW00724 Human but
59	3088	94.7	574	7	ABW00725 Human but
60	3088	94.7	574	8	ADP44738 Human but
61	3088	94.7	574	8	ADRO1055 Human but
62	3088	94.7	574	8	ADRO1061 Human but
63	3088	94.7	574	8	ADRO1065 Human but
64	3088	94.7	574	8	ADRO1071 Human but
65	3088	94.7	574	8	ADRO1069 Human but
66	3087	94.7	574	5	AAOI8978 Human but
67	3087	94.7	574	8	ADRO1063 Human but
68	3087	94.7	574	8	ADRO1043 ButylYich
69	3086	94.7	574	5	AAOI8942 Human but
70	3086	94.7	574	5	AAOI8941 Human but
71	3086	94.7	574	8	ADP44765 Human but
72	3086	94.7	574	8	ADP44821 Human but
73	3086	94.7	574	8	ADRO1057 Human but
74	3086	94.7	574	8	ADRO1067 Human but
75	3085	94.6	574	5	AAOI8899 Human but
76	3085	94.6	574	5	AAOI8943 Human but
77	3085	94.6	574	5	AAOI8901 Human but
78	3085	94.6	574	5	AAOI8902 Human but
79	3085	94.6	574	8	ADP44800 Human but
80	3085	94.6	574	8	ADP44771 Human but
81	3084	94.6	574	5	AAOI8976 Human but
82	3084	94.6	574	8	ADP44776 Human but
83	3084	94.6	574	8	ADP44810 Human but
84	3084	94.6	574	8	ADP44758 Human but
85	3084	94.6	574	8	ADP44780 Human but
86	3084	94.6	574	8	ADP44806 Human but
87	3084	94.6	574	8	ADRO1053 Human but
88	3083	94.6	574	8	ADP44762 Human but
89	3083	94.6	574	8	ADP44769 Human but
90	3083	94.6	574	8	ADP44812 Human but
91	3083	94.6	574	8	ADP44770 Human but
92	3083	94.6	574	8	ADP44755 Human but
93	3083	94.6	574	8	ADP44772 Human but
94	3083	94.6	574	8	ADP44797 Human but
95	3083	94.6	574	8	ADP44739 Human but
96	3083	94.6	574	8	ADP44744 Human but
97	3083	94.6	574	8	ADP44785 Human but
98	3082	94.5	574	5	AAOI8960 Human but

CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 3; Length 602;
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60
 DB 1 MHSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60
 QY 61 YAOPLGLRFRKKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 DB 61 YAOPLGLRFRKKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 QY 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLHVYDGKFLARVERVIVSMYRVGALG 180
 DB 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLHVYDGKFLARVERVIVSMYRVGALG 180
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNIAFGNPKSVTLFGESAGASVSLHLSPG 240
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWOKNIAFGNPKSVTLFGESAGASVSLHLSPG 240
 QY 241 SHSLFTRAILQSGSFNAPWAVTSIYEARNRTLAKLTGCSRENETEIIKLRNKDPOEI 300
 DB 241 SHSLFTRAILQSGSFNAPWAVTSIYEARNRTLAKLTGCSRENETEIIKLRNKDPOEI 300
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQILVGVNKDQGTWFLVY 360
 DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQILVGVNKDQGTWFLVY 360
 QY 361 GAGPFSKDNNSITTRKEFOGLKIFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
 DB 361 GAGPFSKDNNSITTRKEFOGLKIFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
 QY 421 VGDYNTFCPALBETTKFSEWGNNAFFYYFEHRSKLPWPMWGVMGYEIEFVGLPLER 480
 DB 421 VGDYNTFCPALBETTKFSEWGNNAFFYYFEHRSKLPWPMWGVMGYEIEFVGLPLER 480
 QY 481 RDNTYKBEILSRISIVRWANPAKYGNPNETONNSTSPVKSSTOKYLTINTESTRIMT 540
 DB 481 RDNTYKBEILSRISIVRWANPAKYGNPNETONNSTSPVKSSTOKYLTINTESTRIMT 540
 QY 541 KLRAGQCRFWTSFPKYLEMTGNIDEAEWEKAGFHRNNNYMMDKIQFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSFPKYLEMTGNIDEAEWEKAGFHRNNNYMMDKIQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 3
 AA49471
 ID AA49471 standard; protein; 602 AA.

XX AA49471;

XX 27-MAR-2000 (first entry)

XX Human wild-type butyryl cholinesterase (BuChE).

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;

KM butyrylcholinesterase; BuChE; carboxylesterase; Cae; sheep dip; human;

XX nerve agent; organophosphorus acid anhydride; OPAA.

XX US6001625-A.
 PN 14-DEC-1999.
 PD 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 XX (USA) US SEC OF ARMY.
 PA Broomfield CA, Lockridge O, Millard CB;
 PI WPI; 2000-096137/08.
 DR Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 PT Disclosure; Col 3-4; 64pp; English.
 PS The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (Cae)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human Cae). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX Sequence 602 AA;
 QY 1 MDSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60
 DB 1 MHSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60
 QY 61 YAOPLGLRFRKKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 DB 61 YAOPLGLRFRKKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 QY 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLHVYDGKFLARVERVIVSMYRVGALG 180
 DB 121 LYLNWVLPAPKPKNAATLWIYGGGFOTGSSLHVYDGKFLARVERVIVSMYRVGALG 180
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNIAFGNPKSVTLFGESAGASVSLHLSPG 240
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWOKNIAFGNPKSVTLFGESAGASVSLHLSPG 240
 QY 241 SHSLFTRAILQSGSFNAPWAVTSIYEARNRTLAKLTGCSRENETEIIKLRNKDPOEI 300
 DB 241 SHSLFTRAILQSGSFNAPWAVTSIYEARNRTLAKLTGCSRENETEIIKLRNKDPOEI 300
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQILVGVNKDQGTWFLVY 360
 DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKKQILVGVNKDQGTWFLVY 360
 QY 361 GAGPFSKDNNSITTRKEFOGLKIFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
 DB 361 GAGPFSKDNNSITTRKEFOGLKIFPGVSEFGKESILFHYTDWVDDQRPENYREALGDV 420
 QY 421 VGDYNTFCPALBETTKFSEWGNNAFFYYFEHRSKLPWPMWGVMGYEIEFVGLPLER 480
 DB 421 VGDYNTFCPALBETTKFSEWGNNAFFYYFEHRSKLPWPMWGVMGYEIEFVGLPLER 480

Db 421 VGDYNICPALBETKFSWGNNAFFYYFEHRSSKLPWPMWGMVHGIEIEFVGLPLER 480
 QY 481 RDNYTAAEELLSISIVKRWANPAKYGNPNTONNSWSPVFKSTEOKYLTLNTESTRIMT 540
 Db 481 RDNYTAAEELLSISIVKRWANPAKYGNPNTONNSWSPVFKSTEOKYLTLNTESTRIMT 540
 QY 541 KLRAGOCRFMTSPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600
 Db 541 KLRAGOCRFMTSPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600
 QY 601 GL 602
 Db 601 GL 602

RESULT 4
 AAY4573
 ID AAY4573 standard; protein; 602 AA.

AC AAY4573;

DT 04-APR-2000 (first entry)

DE Human wild type Butyrylcholinesterase (BChE) protein.

XX Butyrylcholinesterase; BChE allele; neurological disease; treatment;
 KM therapy; allelic variant; BChE-K; APOE4 allele; neurofibromatosis;
 KM non-AD neurological disease; Alzheimer's disease; Huntington's disease;
 KM depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
 KM Parkinson's disease; multi-infarct dementia; human.

XX Homo sapiens.

XX W09966072-A2.

XX 23-DEC-1999.

XX 16-JUN-1999; 99WO-IB001298.

XX 16-JUN-1998; 98US-0089406P.

XX (NOVA-) NOVA MOLECULAR INC.

XX Sevigny P, Wiebusch H, Schappert K;

XX WPI; 2000-126550/11.

XX N-PSDB; AAZ49470.

XX Prediction of drug efficacy for treating neurological diseases like

XX Alzheimer's disease, neurofibromatosis, Huntington's disease.

XX Example 1, Fig 3; 37pp; English.

XX The present sequence is the wild type human butyrylcholinesterase (BChE)
 CC protein. Determining BChE allele status of a patient helps predicting
 CC risk for neurological diseases, efficacy of therapy and determining
 CC treatment protocol. Presence of BChE allelic variant, BChE-K and APOE4
 CC allele indicate patient's risk for having a neurological disease. This
 CC method enables treating Alzheimer's disease, depression,
 CC neurofibromatosis, Huntington's disease, amyotrophic lateral sclerosis,
 CC multiple sclerosis, stroke, Parkinson's disease, multi-infarct dementia
 CC and other non-AD neurological diseases

XX Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 3; Length 602;

Best Local Similarity 99.7%; Pred. No. 4.3e-287;

Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKTTTICIRFLFWFLMLGKSHEDDIIATKNGKRGKMLTVFGGTVAFGIP 60
 Db 1 MHSKVTIICIRFLFWFLMLGKSHEDDIIATKNGKRGKMLTVFGGTVAFGIP 60

QY 61 VAQPLGLRLFKKPSQSLTKMSDIMNATKXANCCONIDSPFGHSGEMNENTDLSBDC 120
 Db 61 VAQPLGLRLFKKPSQSLTKMSDIMNATKXANCCONIDSPFGHSGEMNENTDLSBDC 120
 QY 121 LYINWITPAPKRNATVLWITYGGRQGTSSLAHYDGFALARVRVYVSNMYVGLG 180
 Db 121 LYINWITPAPKRNATVLWITYGGRQGTSSLAHYDGFALARVRVYVSNMYVGLG 180
 QY 181 FLALPGENPAPGNMGLFDQQLALOWYQKNIAPGNGPKSVTLFGESAGAASVSLHLSBG 240
 Db 181 FLALPGENPAPGNMGLFDQQLALOWYQKNIAPGNGPKSVTLFGESAGAASVSLHLSBG 240
 QY 241 SHSLFTRAILQSGSPNAPWAVTSLYBARNRTLNLAKTGCSRENETEIKCLRNDPOBI 300
 Db 241 SHSLFTRAILQSGSPNAPWAVTSLYBARNRTLNLAKTGCSRENETEIKCLRNDPOBI 300
 QY 301 LLINEAFVVEYGTPLSVNPGPTVDGDELTMDDILELQGFKKTOILVGNKDEGTWFLVY 360
 Db 301 LLINEAFVVEYGTPLSVNPGPTVDGDELTMDDILELQGFKKTOILVGNKDEGTWFLVY 360
 QY 361 GAPGFSKDNNSIITRKEFQEGKIFPPGVSEFGKESILPHYTDWDDQRPENYREALGDV 420
 Db 361 GAPGFSKDNNSIITRKEFQEGKIFPPGVSEFGKESILPHYTDWDDQRPENYREALGDV 420
 QY 421 VGDYNICPALBETKFSWGNNAFFYYFEHRSSKLPWPMWGMVHGIEIEFVGLPLER 480
 Db 421 VGDYNICPALBETKFSWGNNAFFYYFEHRSSKLPWPMWGMVHGIEIEFVGLPLER 480
 QY 481 RDNYTAAEELLSISIVKRWANPAKYGNPNTONNSWSPVFKSTEOKYLTLNTESTRIMT 540
 Db 481 RDNYTAAEELLSISIVKRWANPAKYGNPNTONNSWSPVFKSTEOKYLTLNTESTRIMT 540
 QY 541 KLRAGOCRFMTSPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600
 Db 541 KLRAGOCRFMTSPFKYLEMTGNIDEAEWEMKAGFHRMNNYMMDMKQFNDYTSKESCV 600
 QY 601 GL 602
 Db 601 GL 602

RESULT 5

ABR62392
 ID ABR62392 standard; protein; 602 AA.

AC ABR62392;

DT 03-OCT-2003 (first entry)

DE Human butyrylcholinesterase.

XX Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;

XX EC-3.1.1.8.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..18 /label=Signal_peptide

XX Protein 19..602 /label=Butyrylcholinesterase

XX W02003054182-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-IB005526.

XX 21-DEC-2001; 2001US-0344295P.

XX (NEXT-) NEXIA BIOTECHNOLOGIES INC.

XX Karatzas C, Huang Y, Lazaris A;

XX WPI; 2003-559148/52.
 DR N-PSDB; ACC84170.
 XX New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase
 PT (BChE) enzyme in its milk or urine, useful for large-scale production of
 PT recombinant BChE to prevent or treat organophosphate poisoning or cocaine
 PT intoxication.
 XX Disclousure; Fig 1A; 112pp; English.
 XX The present sequence is the protein sequence of human
 CC butyrylcholinesterase (BChE), including the native signal peptide which
 CC is cleaved during processing to produce the mature BChE protein. The
 CC invention provides methods for large-scale production of recombinant BChE
 CC in cell culture, and in the milk and/or urine of transgenic mammals. The
 CC genome of the transgenic mammal (e.g. goat) comprises a DNA sequence that
 CC encodes BChE operably linked to a mammary gland-specific promoter that
 CC provides secretion of the BChE enzyme into the milk or urine of the
 CC mammal. The recombinant BChE can be used in preventing and/or treating
 CC organophosphate pesticide poisoning, nerve gas poisoning, cocaine
 CC intoxication or succinylcholine-induced apnoea
 CC
 XX
 SQ Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 6; Length 602;
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
 QY 61 YAOPLGRLRFRKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 DB 61 YAOPLGRLRFRKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 QY 121 LYLVNWIIPAKPKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180
 DB 121 LYLVNWIIPAKPKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180
 QY 181 FLALPGNEAPGNGMLFDQDLALQWVKNIAPFGNPKSVTLFGESAGASVSLHLSPG 240
 DB 181 FLALPGNEAPGNGMLFDQDLALQWVKNIAPFGNPKSVTLFGESAGASVSLHLSPG 240
 QY 241 SHSLFTRAIIQSSGFNAPWAVTSLYEARNRTLNAKLTCGSRNETETIIKCLRNKDPOEI 300
 DB 241 SHSLFTRAIIQSSGFNAPWAVTSLYEARNRTLNAKLTCGSRNETETIIKCLRNKDPOEI 300
 QY 301 LINAFAVVPYGTPLSVNPGFTVDDPLTMDPDLLELGQFKKQIILVGVNDEGTAFLVY 360
 DB 301 LINAFAVVPYGTPLSVNPGFTVDDPLTMDPDLLELGQFKKQIILVGVNDEGTAFLVY 360
 QY 361 GAFPSKDNNSIITRKEFOEGIKTFPGVSEFGKESILFHTDWDQRPENTYREALGDV 420
 DB 361 GAFPSKDNNSIITRKEFOEGIKTFPGVSEFGKESILFHTDWDQRPENTYREALGDV 420
 QY 421 VGDYNTICPALEFTKCTSEWGNNAFPYYFEHRSSKLPMEWVGWAGYEIEFVGLPLER 480
 DB 421 VGDYNTICPALEFTKCTSEWGNNAFPYYFEHRSSKLPMEWVGWAGYEIEFVGLPLER 480
 QY 481 RDNTYKAEILSRSTIVRWANFAKGNPNETONNSTGSPVKSTEQKLTINTSTIMT 540
 DB 481 RDNTYKAEILSRSTIVRWANFAKGNPNETONNSTGSPVKSTEQKLTINTSTIMT 540
 QY 541 KLRAGQCRFTWTFPKVLEMTGNIDEAEMWKAQFHRNNYMMDMKQNFNDYTSKESCV 600
 DB 541 KLRAGQCRFTWTFPKVLEMTGNIDEAEMWKAQFHRNNYMMDMKQNFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 6
 ADP90908
 ID ADP90908 standard; protein; 602 AA.
 XX
 AC ADP90908;
 XX

26-FEB-2004 (first entry)

Human hepatic-fibrosis disease marker protein SEQ ID 370.

Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
 hepatic carcinoma; human.

Homo sapiens.

JF2003259877-A.

16-SEP-2003.

11-MAR-2002; 2002JP-00065013.

11-MAR-2002; 2002JP-00065013.

(SUMU) SUMITOMO SEIYAKU KK.

WPI; 2003-821598/77.

Hepatic fibrosis disease markers comprising polynucleotides or
 PT antibodies, useful for improved diagnosis, screening and developing drugs
 PT to treat hepatitis, to control cirrhosis and carcinoma.

Claim 3; SEQ ID NO 370; 313pp; Japanese.

The present invention relates to hepatic-fibrosis disease markers
 CC (ADP90539-ADP90871) and related proteins (ADP90872-ADP90917). The
 CC sequences are useful for detecting and treating hepatic fibrosis caused
 CC by alcohol consumption, virus infection, etc., and the associated chronic
 CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
 CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
 CC precision), so more suitable treatments can be developed and given.

Sequence 602 AA;

Query Match 99.4%; Score 3239; DB 7; Length 602;
 Best Local Similarity 99.7%; Pred. No. 4.3e-287;
 Matches 600; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
 QY 61 YAOPLGRLRFRKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 DB 61 YAOPLGRLRFRKQSLTKMSDIWNAATKANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 QY 121 LYLVNWIIPAKPKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180
 DB 121 LYLVNWIIPAKPKNAATVLIWYGGGFOTGSSLHYVDGKFLARVERIVVSMYRVGALG 180
 QY 181 FLALPGNEAPGNGMLFDQDLALQWVKNIAPFGNPKSVTLFGESAGASVSLHLSPG 240
 DB 181 FLALPGNEAPGNGMLFDQDLALQWVKNIAPFGNPKSVTLFGESAGASVSLHLSPG 240
 QY 241 SHSLFTRAIIQSSGFNAPWAVTSLYEARNRTLNAKLTCGSRNETETIIKCLRNKDPOEI 300
 DB 241 SHSLFTRAIIQSSGFNAPWAVTSLYEARNRTLNAKLTCGSRNETETIIKCLRNKDPOEI 300
 QY 301 LINAFAVVPYGTPLSVNPGFTVDDPLTMDPDLLELGQFKKQIILVGVNDEGTAFLVY 360
 DB 301 LINAFAVVPYGTPLSVNPGFTVDDPLTMDPDLLELGQFKKQIILVGVNDEGTAFLVY 360

QY 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYTDMVDDQRENTREALGV 420
 DB 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYTDMVDDQRENTREALGV 420
 QY 421 VGDYNTFCALPALTETKFSSEWGNNAFFYYFEHRSKSLPPEMGMVHGYEIEFVGLPLER 480
 DB 421 VGDYNTFCALPALTETKFSSEWGNNAFFYYFEHRSKSLPPEMGMVHGYEIEFVGLPLER 480
 QY 481 RDNVTAAEELLSRSIVKRWANFAKYNPNETONNSTSWPVFKSTEOCYLTNTSTRIMT 540
 DB 481 RDNVTAAEELLSRSIVKRWANFAKYNPNETONNSTSWPVFKSTEOCYLTNTSTRIMT 540
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRMNNYMDMKNOFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRMNNYMDMKNOFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 7

AA44574 ID AA44574 standard; protein; 602 AA.

AA44574;

04-APR-2000 (first entry)

Human Butyrylcholinesterase-K (BChE-K) protein.

Butyrylcholinesterase-K; BChE-K; BChE allele; neurological disease;
 therapy; treatment; allelic variant; apoE4 allele; neurofibromatosis;
 non-AD neurological disease; Alzheimer's disease; Huntington's disease;
 depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
 Parkinson's disease; multi-infarct dementia; human.

Homo sapiens.

OS Homo sapiens.

EH Key location/Qualifiers

FT Misc-difference 567

PD 23-DEC-1999.

XX 16-JUN-1999; 99WO-IB001298.

XX 16-JUN-1998; 98US-0089406P.

XX (NOVA-) NOVA MOLECULAR INC.

XX Seviigny P, Wiebusch H, Schappert K;

XX MPI, 2000-126550/11.

XX N-PSDB; AA249471.

XX Prediction of drug efficacy for treating neurological diseases like

XX Alzheimer's disease, neurofibromatosis, Huntington's disease.

XX Disclosure; Fig 4; 37p; English.

XX The present sequence is the human polymorphic variant
 CC butyrylcholinesterase-K (BChE-K) protein. BChE-K is an allelic variant of
 CC BChE. Determining BChE allele status (homozygous or heterozygous) of a
 CC patient helps predicting risk of neurological diseases, efficacy of
 CC therapy and determining treatment protocol. BChE-K and apoE4 allele
 CC status also indicate patient's risk for having a neurological disease.
 CC This method enables treating Alzheimer's disease, Huntington's disease,
 CC depression, neurofibromatosis, amyotrophic lateral sclerosis, stroke,
 CC multiple sclerosis, Parkinson's disease, multi-infarct dementia and other
 CC non-AD neurological diseases

XX Sequence 602 AA;

Query Match 99.2%; Score 3235; DB 3; Length 602;
 Best Local Similarity 99.5%; Pred. No. 1e-286;
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTIIICIRLFWFLMLIGKSHTEDDIIITKNGKRGKMLTVFGTVAFLGIP 60
 DB 1 MDSKVTIIICIRLFWFLMLIGKSHTEDDIIITKNGKRGKMLTVFGTVAFLGIP 60
 QY 61 YVQPLGRILRFKPKQSLTWSMDIWNATKXANCCNIDQSPFGFSGSEMMNNTLSDDC 120
 DB 61 YVQPLGRILRFKPKQSLTWSMDIWNATKXANCCNIDQSPFGFSGSEMMNNTLSDDC 120
 QY 121 LYINWVTPAPKPKNTVLIMVIGGGFQGTSSLAHYDGFKLARVRVIVSNMYVGAIG 180
 DB 121 LYINWVTPAPKPKNTVLIMVIGGGFQGTSSLAHYDGFKLARVRVIVSNMYVGAIG 180
 QY 181 FLALPGRNPEAPGNMGLFDQQLALQWYOKNIAAFGNGPKSVTLFGESAGAAVSJHLSPG 240
 DB 181 FLALPGRNPEAPGNMGLFDQQLALQWYOKNIAAFGNGPKSVTLFGESAGAAVSJHLSPG 240
 QY 241 SHSLFTRALLOSQSFPAWPAVTSIYEARRTNLAKLGCSENETEIIKCLRNDPOEI 300
 DB 241 SHSLFTRALLOSQSFPAWPAVTSIYEARRTNLAKLGCSENETEIIKCLRNDPOEI 300
 QY 301 LINEAFVVEYGTPLSVNFGPTVDGDFLTDMPDILLELQGFKKTQILLVGNKDEGTWFLVY 360
 DB 301 LINEAFVVEYGTPLSVNFGPTVDGDFLTDMPDILLELQGFKKTQILLVGNKDEGTWFLVY 360
 QY 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYTDMVDDQRENTREALGV 420
 DB 361 GAFGFSKDNNSITTRKEFOGGLKIFPPGVSEFGKESILFHYTDMVDDQRENTREALGV 420
 QY 421 VGDYNTFCALPALTETKFSSEWGNNAFFYYFEHRSKSLPPEMGMVHGYEIEFVGLPLER 480
 DB 421 VGDYNTFCALPALTETKFSSEWGNNAFFYYFEHRSKSLPPEMGMVHGYEIEFVGLPLER 480
 QY 481 RDNVTAAEELLSRSIVKRWANFAKYNPNETONNSTSWPVFKSTEOCYLTNTSTRIMT 540
 DB 481 RDNVTAAEELLSRSIVKRWANFAKYNPNETONNSTSWPVFKSTEOCYLTNTSTRIMT 540
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRMNNYMDMKNOFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRMNNYMDMKNOFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 8

AA449483 ID AA449483 standard; protein; 602 AA.

AA449483;

27-MAR-2000 (first entry)

Human butyryl cholinesterase (BuChE) mutant.

Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 butyrylcholinesterase; BuChE; carboxylesterase; Ca; sheep dip; human;
 nerve agent; organophosphorus acid anhydride; OPAA; mutant.

Homo sapiens.

Synthetic.

US6001625-A.

14-DEC-1999.

PF 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 XX (USA) US SEC OF ARMY.
 PA Broomfield CA, Lockridge O, Millard CB;
 PT WPI; 2000-096137/08.
 XX
 XX
 PT Enhancing the organophosphate detoxifying capabilities of esterases for
 the treatment of organophosphate poisoning.
 PS Disclosure; Col 9-10; 64pp; English.
 XX
 XX The invention provides a method of enhancing organophosphate detoxifying
 capabilities of esterases (either human acetylcholinesterases (ACHE), that
 human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 comprises substituting an active site residue for 1 or more amino acid(s)
 within 6 Angstrom of an active site residue. The method may be used for
 enhancing organophosphate detoxifying capabilities of esterases (either
 human ACHE, human BuChE and/or human CaE). The modified esterases may
 then be used to treat agricultural workers poisoned with organophosphates
 through contact with chemical such as sheep dips. They may also be used
 to treat military personnel contaminated by chemical weapons such as
 nerve agents. Additionally, the esterases may also be used to
 decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 SQ Sequence 602 AA;

Query Match 99.2%; Score 3234; DB 3; Length 602;
 Best Local Similarity 99.5%; Pred. No. 1,2e-286;
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTITICRFLFWFLLCMLIGKSHTEDEIIATKNGKRVGNMLFVGGTVAFLGIP 60
 DB 1 MHSKVTITICRFLFWFLLCMLIGKSHTEDEIIATKNGKRVGNMLFVGGTVAFLGIP 60
 QY 61 YAOPLRLRREKQSLTKMSDINWATKYANSCONIDQSPFGHSGEMNPNITLSEDC 120
 DB 61 YAOPLRLRREKQSLTKMSDINWATKYANSCONIDQSPFGHSGEMNPNITLSEDC 120
 QY 121 LYLNWMIAPKPKKATVLIWYGGGFGTGTSSLHVYDGKFLARYERYIVVSMNRYVAGLG 180
 DB 121 LYLNWMIAPKPKKATVLIWYGGGFGTGTSSLHVYDGKFLARYERYIVVSMNRYVAGLG 180
 QY 121 LYLNWMIAPKPKKATVLIWYGGGFGTGTSSLHVYDGKFLARYERYIVVSMNRYVAGLG 180
 DB 121 LYLNWMIAPKPKKATVLIWYGGGFGTGTSSLHVYDGKFLARYERYIVVSMNRYVAGLG 180
 QY 181 FLALPGNPEAPGNNGLFDQOLALQWVQNTAIPGNPKSVTLPEESAGASVSLHLSPG 240
 DB 181 FLALPGNPEAPGNNGLFDQOLALQWVQNTAIPGNPKSVTLPEESAGASVSLHLSPG 240
 QY 241 SHSLFTTALLOSQSGFNAPWATVSLYEARNRTLNIAKLTCGRENEMTEIIKLRKNDPOEI 300
 DB 241 SHSLFTTALLOSQSGFNAPWATVSLYEARNRTLNIAKLTCGRENEMTEIIKLRKNDPOEI 300
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELGGQFKTQIILGVNKGDEGTFLVY 360
 DB 301 LLINEAFVVPYGTPLSVNFGPTVDGFLTMDPDLLELGGQFKTQIILGVNKGDEGTFLVY 360
 QY 361 GAFGFSKDNNSIIRKKEFOEGKIFPPGVSEFGKESILFHTDWDVDDORPNRYEALGDV 420
 DB 361 GAFGFSKDNNSIIRKKEFOEGKIFPPGVSEFGKESILFHTDWDVDDORPNRYEALGDV 420
 QY 421 VGDYNTICPALFETKSEWGNNAFFYYFEHRSKSLPMEWMVGMHGEIEFVGLPLER 480
 DB 421 VGDYNTICPALFETKSEWGNNAFFYYFEHRSKSLPMEWMVGMHGEIEFVGLPLER 480
 QY 481 RDNVTKAEILSRIVKMANFACYGNPNETQNNSTWSPVFKSTEOXYTLTNTSTIMT 540
 DB 481 RDNVTKAEILSRIVKMANFACYGNPNETQNNSTWSPVFKSTEOXYTLTNTSTIMT 540

QY 541 KLRAGQCRFWTSFPPKYLENTGNIDEAEWEMKAGFHEMNMYMDWKNQFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSFPPKYLENTGNIDEAEWEMKAGFHEMNMYMDWKNQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 9
 ID AAR37442 standard; protein; 602 AA.
 AC AAR37442;
 DT 25-MAR-2003 (revised)
 DT 06-OCT-1993 (first entry)
 XX Full-length human pseudocholinesterase.
 XX butyrylcholinesterase; acylcholine acylhydrolase; EC3.1.1.8; psi-ChE;
 KM pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;
 KM antitoxin.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT /note= "putative leader peptide"
 FT /note= "45..47"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT /note= "134..136"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT /note= "226"
 FT Active-site
 FT /note= "active site Serine"
 FT /note= "269..271"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT /note= "284..286"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT /note= "369..371"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT /note= "509..511"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 FT /note= "514..516"
 FT Modified-site
 FT /note= "potential N-glycosylation site"
 XX US5215909-A.
 XX 01-JUN-1993.
 XX 15-AUG-1990; 90US-00572911.
 XX 18-JUN-1986; 86US-00875737.
 XX 21-AUG-1987; 87US-00087724.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX Soreq H;
 PT WPI; 1993-188509/23.
 DR N-PSDB; AAQ42496.
 XX Recombinant human gene encoding human pseudo-cholinesterase - used to
 PT treat organo-phosphorus poisoning.
 XX Disclosure; Col 35-40; 34pp; English.
 XX A cDNA library prepared from foetal brain mRNA was screened with
 CC degenerate probe pools based on the organophosphorus binding site of
 CC cholinesterases. A 764 nucleotide insert (designated FCBH12) was
 CC isolated from one positive clone and sequenced. This insert (AAQ42495),
 CC containing an ORF large enough to code for about half the subunit size of

CC human cholinesterase, was used as a probe to obtain the full-length
 CC pseudocholinesterase sequence (AA042496). (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 602 AA;

Query Match 99.2%; Score 3233; DB 2; Length 602;

Best Local Similarity 99.5%; Pred. No. 1.5e-286;

Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MDSKVTIIICIRLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVEGTVATFLGIP 60
DB 1 MHSKVTIIICIRLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVEGTVATFLGIP 60
QY 61 YAOPLGRLEFRKPKOSLTKMSDIWNAKYANSCCONIDSPFGHSEMMNPNTDISEDC 120
DB 61 YAOPLGRLEFRKPKOSLTKMSDIWNAKYANSCCONIDSPFGHSEMMNPNTDISEDC 120
QY 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVSMYRVGALG 180
DB 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVSMYRVGALG 180
QY 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAGGNPKSVTLFGESAGAASVSLHLLSPG 240
DB 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAGGNPKSVTLFGESAGAASVSLHLLSPG 240
QY 241 SHSLFTTRAILIQQSGSFNAPMAVTSIYEARNRTLNALKTGSRRENETIICKLRKDPQEI 300
DB 241 SHSLFTTRAILIQQSGSFNAPMAVTSIYEARNRTLNALKTGSRRENETIICKLRKDPQEI 300
QY 301 LLINEAFVVPYGPPLSVNFGPTVDGFLTMDPDLLELGQPKTQILVGNKDEGTWFLVY 360
DB 301 LLINEAFVVPYGPPLSVNFGPTVDGFLTMDPDLLELGQPKTQILVGNKDEGTWFLVY 360
QY 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRENYREALGDV 420
DB 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRENYREALGDV 420
QY 421 VGDYNIICPALFETFKFSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480
DB 421 VGDYNIICPALFETFKFSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480
QY 481 RDNYTKAEILSRISIVRWANFAKYGNPNETONNSTMPVFKSTEQKYLTLNTESTRIMT 540
DB 481 RDNYTKAEILSRISIVRWANFAKYGNPNETONNSTMPVFKSTEQKYLTLNTESTRIMT 540
QY 541 KLRAGOCRFMTSFPKYLLEMTGNIDEAEWEWKAGFHRMNNYMDWKNQFNDYTSKESCV 600
DB 541 KLRAGOCRFMTSFPKYLLEMTGNIDEAEWEWKAGFHRMNNYMDWKNQFNDYTSKESCV 600
QY 601 GL 602
DB 601 GL 602

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RESULT 10

AAV49474 ID AAV49474 standard; protein; 602 AA.

XX AAV49474;

DT 27-MAR-2000 (first entry)

XX Human butyryl cholinesterase (BuChE) mutant.

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KM butyrylcholinesterase; BuChE; carboxylesterase; Car; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.

OS Homo sapiens.

XX Synthetic.

PN US6001625-A.

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XX 14-DEC-1999.
PD 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
PA (USSA ) US SEC OF ARMY.
PI Broomfield CA, Lockridge O, Millard CB;
PI WPI; 2000-096137/08.
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
PS Disclosure; Col 3-6; 64pp; English.
XX The invention provides a method of enhancing organophosphate detoxifying
XX capabilities of esterases (either human acetylcholinesterases (AChE), that
XX human butyrylcholinesterases (BuChE) and/or carboxylesterases (Car)), that
XX comprises substituting a histidine residue for 1 or more amino acid(s)
XX within 6 Angstrom of an active site serine. The method may be used for
XX enhancing organophosphate detoxifying capabilities of esterases (either
XX human AChE, human BuChE and/or human Car). The modified esterases may
XX then be used to treat agricultural workers poisoned with organophosphates
XX through contact with chemical such as sheep dips. They may also be used
XX to treat military personnel contaminated by chemical weaponry such as
XX nerve agents. Additionally, the esterases may also be used to
XX decontaminate ground and buildings and equipment used to store, or
XX contaminated by organophosphates. The method produces esterases with
XX improved detoxification properties over naturally occurring
XX organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
XX less likely to be inactivated by the OPAA
XX
SQ Sequence 602 AA;

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Query Match 99.1%; Score 3232; DB 3; Length 602;

Best Local Similarity 99.5%; Pred. No. 1.9e-286;

Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MDSKVTIIICIRLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVEGTVATFLGIP 60
DB 1 MHSKVTIIICIRLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVEGTVATFLGIP 60
QY 61 YAOPLGRLEFRKPKOSLTKMSDIWNAKYANSCCONIDSPFGHSEMMNPNTDISEDC 120
DB 61 YAOPLGRLEFRKPKOSLTKMSDIWNAKYANSCCONIDSPFGHSEMMNPNTDISEDC 120
QY 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVSMYRVGALG 180
DB 121 LYLNWMIAPKPKNAATVLIWYGGGFOTGTSLSHVDGKFLARVERIVVSMYRVGALG 180
QY 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAGGNPKSVTLFGESAGAASVSLHLLSPG 240
DB 181 FLALPGNPEAPGNMGLFDQOLALQWQKNTAAGGNPKSVTLFGESAGAASVSLHLLSPG 240
QY 241 SHSLFTTRAILIQQSGSFNAPMAVTSIYEARNRTLNALKTGSRRENETIICKLRKDPQEI 300
DB 241 SHSLFTTRAILIQQSGSFNAPMAVTSIYEARNRTLNALKTGSRRENETIICKLRKDPQEI 300
QY 301 LLINEAFVVPYGPPLSVNFGPTVDGFLTMDPDLLELGQPKTQILVGNKDEGTWFLVY 360
DB 301 LLINEAFVVPYGPPLSVNFGPTVDGFLTMDPDLLELGQPKTQILVGNKDEGTWFLVY 360
QY 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRENYREALGDV 420
DB 361 GADPFSKDNNSITTRKEFOEGKIFPPGVSEFKESILFHYTDWDDQRENYREALGDV 420
QY 421 VGDYNIICPALFETFKFSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480
DB 421 VGDYNIICPALFETFKFSEWGNNAFFYYFEHRSSKLPWPEMGMVHGYEIEFVFGPLER 480

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QY 481 RDNTYKAEILSRISIVKMANFAKGNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540
 DB 481 RDNTYKAEILSRISIVKMANFAKGNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540
 QY 541 KLRQOQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDWKQFNDYTSKESCV 600
 DB 541 KLRQOQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDWKQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 11
 ID AAY49473 standard; protein; 602 AA.
 AC AAY49473;

DT 27-MAR-2000 (first entry)
 XX Human butyryl cholinesterase (BuChE) mutant.
 DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaB; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX

OS Homo sapiens.
 OS Synthetic.
 PN US6001625-A.
 PD 14-DEC-1999.
 XX 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 PA (USSA) US SEC OF ARMY.

PI Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 PT Enhancing the organophosphate detoxifying capabilities of esterases for
 the treatment of organophosphate poisoning.

PS Disclosure; Col 3-4; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaB)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaB). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.1%; Score 3232; DB 3; Length 602;
 Best Local Similarity 99.5%; Pred. No. 1.9e-286;
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTITICRFLFWPILLCLMLIGKSHTEBDIIATKNGKVRGNLTVFGTVAFAFGIP 60

DB 1 MHSKVTITICRFLFWPILLCLMLIGKSHTEBDIIATKNGKVRGNLTVFGTVAFAFGIP 60
 QY 61 YAOPLGRLEAFKKPOSTLTKMSDIWNATKYANSCCONIDQSPGPHGSEMMNPNTDLSDDC 120
 DB 61 YAOPLGRLEAFKKPOSTLTKMSDIWNATKYANSCCONIDQSPGPHGSEMMNPNTDLSDDC 120
 QY 121 LYNWMIAPKPKRNATVLIWYGGGFGTGSLSHYDGKFLAVERVIVSMYRVGALG 180
 DB 121 LYNWMIAPKPKRNATVLIWYGGGFGTGSLSHYDGKFLAVERVIVSMYRVGALG 180
 QY 181 FLALPGNPEAPGNWGLFDQOLALQWOKNTAARGNPKSYTLFGESGAASVSLHLISPG 240
 DB 181 FLALPGNPEAPGNWGLFDQOLALQWOKNTAARGNPKSYTLFGESGAASVSLHLISPG 240
 QY 241 SHSLFTRAILQSGSFNAPMAVTSIYEARNRTLMLAKLTGCSRENETIILCLRNKDPOEI 300
 DB 241 SHSLFTRAILQSGSFNAPMAVTSIYEARNRTLMLAKLTGCSRENETIILCLRNKDPOEI 300
 QY 301 LLINEAFVVPYGTPLSVNFGFTVDGDLTDMPDILLLEIGQPKKQIILGVNKBEGTWPLVY 360
 DB 301 LLINEAFVVPYGTPLSVNFGFTVDGDLTDMPDILLLEIGQPKKQIILGVNKBEGTWPLVY 360
 QY 361 GARGFSKDNNSITTRKEFGGLKIFPPGVSEFGKESILFHYTDWDDQRENTREALGDV 420
 DB 361 GARGFSKDNNSITTRKEFGGLKIFPPGVSEFGKESILFHYTDWDDQRENTREALGDV 420
 QY 421 VGDYNFICPALFETKKESEWGNNAFFYPFHRSSKLPMPMWGMVGHYELEFPVGLER 480
 DB 421 VGDYNFICPALFETKKESEWGNNAFFYPFHRSSKLPMPMWGMVGHYELEFPVGLER 480
 QY 481 RDNTYKAEILSRISIVKMANFAKGNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540
 DB 481 RDNTYKAEILSRISIVKMANFAKGNPNETONNSTSWPVFKSTEQKYLTLNTESTRIMT 540
 QY 541 KLRQOQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDWKQFNDYTSKESCV 600
 DB 541 KLRQOQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRMNNYMDWKQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 12
 ID AAY49475 standard; protein; 602 AA.
 AC AAY49475;

DT 27-MAR-2000 (first entry)
 XX Human butyryl cholinesterase (BuChE) mutant.

DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaB; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.

OS Homo sapiens.
 OS Synthetic.

PN US6001625-A.
 PD 14-DEC-1999.
 XX 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.

PA (USSA) US SEC OF ARMY.
 PI Broomfield CA, Lockridge O, Millard CB;

DR WPI; 2000-096137/08.

XX Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
XX

PS Disclosure; Col 5-6; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE), that
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX

SO Sequence 602 AA:

Query Match 99.1%; Score 3232; DB 3; Length 602;
Best Local Similarity 99.5%; Pred. No. 1.9e-286;
Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
QY 61 YAOPLGLRLFRFKPKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
DB 61 YAOPLGLRLFRFKPKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
QY 121 LYANWIPAPRKPAKTVLIMTYGGGFGORTSSLIHYDGKFLARVERVIVSMNTRVGLG 180
DB 121 LYANWIPAPRKPAKTVLIMTYGGGFGORTSSLIHYDGKFLARVERVIVSMNTRVGLG 180
QY 121 LYANWIPAPRKPAKTVLIMTYGGGFGORTSSLIHYDGKFLARVERVIVSMNTRVGLG 180
DB 121 LYANWIPAPRKPAKTVLIMTYGGGFGORTSSLIHYDGKFLARVERVIVSMNTRVGLG 180
QY 181 FLALPGNPEAPGNMGLPQOLALQWQKNIAGFGNPKSVTLFGESAGASVSLHLSPG 240
DB 181 FLALPGNPEAPGNMGLPQOLALQWQKNIAGFGNPKSVTLFGESAGASVSLHLSPG 240
QY 181 FLALPGNPEAPGNMGLPQOLALQWQKNIAGFGNPKSVTLFGESAGASVSLHLSPG 240
DB 181 FLALPGNPEAPGNMGLPQOLALQWQKNIAGFGNPKSVTLFGESAGASVSLHLSPG 240
QY 241 SHSLFTRAIILOGSFNAFWAVTSIYEARNRITLAKLTGCSRENETEIKICLRNKDPOEI 300
DB 241 SHSLFTRAIILOGSFNAFWAVTSIYEARNRITLAKLTGCSRENETEIKICLRNKDPOEI 300
QY 241 SHSLFTRAIILOGSFNAFWAVTSIYEARNRITLAKLTGCSRENETEIKICLRNKDPOEI 300
DB 241 SHSLFTRAIILOGSFNAFWAVTSIYEARNRITLAKLTGCSRENETEIKICLRNKDPOEI 300
QY 301 LLNNAFVVPYGTPLSVNFGPMDGDLTMDPILILEGPKKTOILVGNKDEGTWFLVY 360
DB 301 LLNNAFVVPYGTPLSVNFGPMDGDLTMDPILILEGPKKTOILVGNKDEGTWFLVY 360
QY 301 LLNNAFVVPYGTPLSVNFGPMDGDLTMDPILILEGPKKTOILVGNKDEGTWFLVY 360
DB 301 LLNNAFVVPYGTPLSVNFGPMDGDLTMDPILILEGPKKTOILVGNKDEGTWFLVY 360
QY 361 GAPGSKNNNSIITTKRFOEGIKIFPPGVSEFGKESILFHYTDWVDORPENYRRLADGV 420
DB 361 GAPGSKNNNSIITTKRFOEGIKIFPPGVSEFGKESILFHYTDWVDORPENYRRLADGV 420
QY 421 VGDYNPICPALFTTKKFSFEMGNNAFFYFHRSSKLPEPMWGVHGEIEBVFSLPLER 480
DB 421 VGDYNPICPALFTTKKFSFEMGNNAFFYFHRSSKLPEPMWGVHGEIEBVFSLPLER 480
QY 481 RNNYKABEILRSIYKRWANPAKGNPETONNSTSWPFSTOKLTLNTESSTRIMT 540
DB 481 RNNYKABEILRSIYKRWANPAKGNPETONNSTSWPFSTOKLTLNTESSTRIMT 540
QY 481 RNNYKABEILRSIYKRWANPAKGNPETONNSTSWPFSTOKLTLNTESSTRIMT 540
DB 481 RNNYKABEILRSIYKRWANPAKGNPETONNSTSWPFSTOKLTLNTESSTRIMT 540
QY 541 KLRAGQCRFTWTFPPVLEMTGNIDAEWEMKAGFHRNNVMMDWKQNFNDYTSKESCV 600
DB 541 KLRAGQCRFTWTFPPVLEMTGNIDAEWEMKAGFHRNNVMMDWKQNFNDYTSKESCV 600
QY 601 GL 602
DB 601 GL 602

RESULT 13

AA49472
ID AA49472 standard; protein; 602 AA.

AA49472;

27-MAR-2000 (first entry)

Human butyryl cholinesterase (BuChE) mutant G117H.

Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
nerve agent; organophosphorus acid anhydride; OPAA; mutant.

Homo sapiens.
Synthetic.

Key Location/Qualifiers
Misc-difference 145 /note="wild-type Gly is replaced with His"

US6001625-A.

14-DEC-1999.

19-MAY-1995; 95US-00446100.

19-MAY-1995; 95US-00446100.

(USSA) US SEC OF ARMY.

Broomfield CA, Lockridge O, Millard CB;

WPI; 2000-096137/08.

Enhancing the organophosphate detoxifying capabilities of esterases for
the treatment of organophosphate poisoning.

Claim 10; Col 123-126; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE), that
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX

SO Sequence 602 AA:

Query Match 99.1%; Score 3231; DB 3; Length 602;
Best Local Similarity 99.5%; Pred. No. 2.3e-286;
Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVTAFLGIP 60
QY 61 YAOPLGLRLFRFKPKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
DB 61 YAOPLGLRLFRFKPKQSLTKMSDIMNATKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120

QY 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNTRVAGLG 180
Db 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNTRVAGLG 180
QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGAAVSLSHLSPG 240
Db 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGAAVSLSHLSPG 240
QY 241 SHSLFTRAIIQSOSFNAPMAVTSLEYARNRTLNATKTCGRNETETIICLRKNDPOEI 300
Db 241 SHSLFTRAIIQSOSFNAPMAVTSLEYARNRTLNATKTCGRNETETIICLRKNDPOEI 300
QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQGFKTKQIILVGNKDEGTWFLVY 360
Db 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQGFKTKQIILVGNKDEGTWFLVY 360
QY 361 GARGFSKDNNSITTRKSFQEGKIFPPGVSEFGKESILFHYTWDVDDQRPENTYREALGDV 420
Db 361 GARGFSKDNNSITTRKSFQEGKIFPPGVSEFGKESILFHYTWDVDDQRPENTYREALGDV 420
QY 421 VGDYNFICPALFETTKFSEWGNNAFFYFPHRSSKLPMPWGMVGMGEIEFVGLPLER 480
Db 421 VGDYNFICPALFETTKFSEWGNNAFFYFPHRSSKLPMPWGMVGMGEIEFVGLPLER 480
QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTMPVEKSTQKYLTLNTESTRIMT 540
Db 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTMPVEKSTQKYLTLNTESTRIMT 540
QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDMKNQFNDYTSKESCV 600
Db 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDMKNQFNDYTSKESCV 600
QY 601 GL 602
Db 601 GL 602

RESULT 14
ID AAY49476 standard; protein; 602 AA.
AC AAY49476;
XX 27-MAR-2000 (first entry)
DT XX
XX Human butyryl cholinesterase (BuChE) mutant.
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
XX butyrylcholinesterase; BuChE; carboxylesterase; CaB; sheep dip; human;
XX nerve agent; organophosphorus acid anhydride; OPA; mutant.
OS Homo sapiens.
OS Synthetic.
XX US6001625-A.
XX 14-DEC-1999.
XX 19-MAY-1995; 95US-00446100.
XX 19-MAY-1995; 95US-00446100.
XX (USSA) US SEC OF ARMY.
XX Broomfield CA, Lockridge O, Millard CB;
XX WPI; 2000-096137/08.
XX Enhancing the organophosphate detoxifying capabilities of esterases for
XX the treatment of organophosphate poisoning.
XX Disclosure; Col 5-6; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaB)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaB). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPA
XX
SQ Sequence 602 AA;
Query Match 99.1%; Score 3231; DB 3; Length 602;
Best Local Similarity 99.5%; Pred. No. 2,3e-286;
Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDSKVTIICIRPLFWPLLCMLIGKSHTEBDIIATKNGKVRGMNLTVEGCTYAFIGIP 60
Db 1 MHSKVTIICIRPLFWPLLCMLIGKSHTEBDIIATNGVCRGMNLTVEGCTYAFIGIP 60
QY 61 YAPPLGRLEFPKPOSITTKMSDINATKYANSCCONIDQFPFGHSEMNPNTDSEDC 120
Db 61 YAPPLGRLEFPKPOSITTKMSDINATKYANSCCONIDQFPFGHSEMNPNTDSEDC 120
QY 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNTRVAGLG 180
Db 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERVIVSMNTRVAGLG 180
QY 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGAAVSLSHLSPG 240
Db 181 FLALPGNPEAPGNMGLFDQOLALQWOKNTAAFGNPKSVTLFGESAGAAVSLSHLSPG 240
QY 241 SHSLFTRAIIQSOSFNAPMAVTSLEYARNRTLNATKTCGRNETETIICLRKNDPOEI 300
Db 241 SHSLFTRAIIQSOSFNAPMAVTSLEYARNRTLNATKTCGRNETETIICLRKNDPOEI 300
QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQGFKTKQIILVGNKDEGTWFLVY 360
Db 301 LNEAFVVPYGTPLSVNFGPTVDGFLTDMPDILLELQGFKTKQIILVGNKDEGTWFLVY 360
QY 361 GARGFSKDNNSITTRKSFQEGKIFPPGVSEFGKESILFHYTWDVDDQRPENTYREALGDV 420
Db 361 GARGFSKDNNSITTRKSFQEGKIFPPGVSEFGKESILFHYTWDVDDQRPENTYREALGDV 420
QY 421 VGDYNFICPALFETTKFSEWGNNAFFYFPHRSSKLPMPWGMVGMGEIEFVGLPLER 480
Db 421 VGDYNFICPALFETTKFSEWGNNAFFYFPHRSSKLPMPWGMVGMGEIEFVGLPLER 480
QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTMPVEKSTQKYLTLNTESTRIMT 540
Db 481 RDNVTKAEILSRISIVKRWANPAKYGNPNETONNSTMPVEKSTQKYLTLNTESTRIMT 540
QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDMKNQFNDYTSKESCV 600
Db 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRNNYMDMKNQFNDYTSKESCV 600
QY 601 GL 602
Db 601 GL 602

RESULT 15
ID AAY49477 standard; protein; 602 AA.
AC AAY49477;
XX

XX 27-MAR-2000 (first entry)
 DT Human butyryl cholinesterase (BuChE) mutant.
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 XX butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX Homo sapiens.
 OS Synthetic.
 XX US6001625-A.
 PN 14-DEC-1999.
 PD 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 PR (USSA) US SEC OF ARMY.
 PA Broomfield CA, Lockridge O, Millard CB;
 PI WPI; 2000-096137/08.
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 DR Disclosure; Col 5-6; 64pp; English.
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 CC
 XX Sequence 602 AA;
 SQ
 Query Match 99.1%; Score 3230; DB 3; Length 602;
 Best Local Similarity 99.5%; Pred. No. 2.9e-266;
 Matches 599; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 LINEAFVVPYGTPLSNRGPVVDGDFLMDPILILELQCFKKTQILVGVNKGDTWFLVY 360
 DB 301 LINEAFVVPYGTPLSNRGPVVDGDFLMDPILILELQCFKKTQILVGVNKGDTWFLVY 360
 QY 361 GAPPSEKDNNSIITRKEFOEGLKIFPPGVSEFGKESILFHYTDWYDDQRPENYREALGVY 420
 DB 361 GAPPSEKDNNSIITRKEFOEGLKIFPPGVSEFGKESILFHYTDWYDDQRPENYREALGVY 420
 QY 421 VGDYNTCPALERTKSPSEWGNNAFFPYEHHSSKLPMPENMGVNHGIEEVPGLPLER 480
 DB 421 VGDYNTCPALERTKSPSEWGNNAFFPYEHHSSKLPMPENMGVNHGIEEVPGLPLER 480
 QY 481 RDNVTAEBILSRSIYKRWANPAKGNPNETONNSTSWPFKSTQKYLTLNTESTRIWT 540
 DB 481 RDNVTAEBILSRSIYKRWANPAKGNPNETONNSTSWPFKSTQKYLTLNTESTRIWT 540
 QY 541 KLRAGQCRFTWTSPPKRYLMTGNIDAEWEMKAGHRRNNYMMDKQNDYTSKESCV 600
 DB 541 KLRAGQCRFTWTSPPKRYLMTGNIDAEWEMKAGHRRNNYMMDKQNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602
 DB 601 GL 602
 RESULT 16
 ID AAY49484
 ID AAY49484 standard; protein; 602 AA.
 AC AAY49484;
 XX 27-MAR-2000 (first entry)
 DT Human butyryl cholinesterase (BuChE) mutant.
 DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 XX butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX Homo sapiens.
 OS Synthetic.
 XX US6001625-A.
 PN 14-DEC-1999.
 PD 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 PA (USSA) US SEC OF ARMY.
 PI Broomfield CA, Lockridge O, Millard CB;
 PI WPI; 2000-096137/08.
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 DR Disclosure; Col 9-10; 64pp; English.
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to

CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.0%; Score 3228; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 4.4e-286;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGKGNLTVFGSTVAFIIGIP 60
 DB 1 MHSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGKGNLTVFGSTVAFIIGIP 60
 QY 61 YAOPLGLRLRPFKKPOSITKMSDIWNATKYANSCCQNDQSPFGHSEMNPNPTDLSBDC 120
 DB 61 YAOPLGLRLRPFKKPOSITKMSDIWNATKYANSCCQNDQSPFGHSEMNPNPTDLSBDC 120
 QY 121 LYLNVWIPARKPKNAATVLIWIIYGGGFCOTGTSLSHVYDGKFLARVERVIVSMNRYVAGALG 180
 DB 121 LYLNVWIPARKPKNAATVLIWIIYGGGFCOTGTSLSHVYDGKFLARVERVIVSMNRYVAGALG 180
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWVQKNTAAFGGNPKSVTLFGESAGAASVSHLLSPG 240
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWVQKNTAAFGGNPKSVTLFGESAGAASVSHLLSPG 240
 QY 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPOEI 300
 DB 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPOEI 300
 QY 301 LLINEAFVVPYGTPLSVNPGFTVNDGFLTMDPDLLELGQFKKQIILVGNKDEGTWFLVY 360
 DB 301 LLINEAFVVPYGTPLSVNPGFTVNDGFLTMDPDLLELGQFKKQIILVGNKDEGTWFLVY 360
 QY 361 GAGPFSKDNNSITTRKEFOGLKIFPPGVSEFKESILFHTDWVDDQRPENYREALGDV 420
 DB 361 GAGPFSKDNNSITTRKEFOGLKIFPPGVSEFKESILFHTDWVDDQRPENYREALGDV 420
 QY 421 VGDYNIICPALFETKKESEKNNAPFYFFHRSSKLPPEMVGWGHYEIEFVGLPLER 480
 DB 421 VGDYNIICPALFETKKESEKNNAPFYFFHRSSKLPPEMVGWGHYEIEFVGLPLER 480
 QY 481 RDNITKABEILSRISIVKMANFAKYGNPNETQNNSTSPVFKSTEOKYLTLNTESTRIIMT 540
 DB 481 RDNITKABEILSRISIVKMANFAKYGNPNETQNNSTSPVFKSTEOKYLTLNTESTRIIMT 540
 QY 541 KLRAGQCRFWTSFPKVLKEMTGNIDEAEWEMKAGFHRNNNTMDMKQFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSFPKVLKEMTGNIDEAEWEMKAGFHRNNNTMDMKQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 17

AAV49478 ID AAV49478 standard; protein; 602 AA.

XX AC AAV49478;

XX DT 27-MAR-2000 (first entry)

XX DE Human butyryl cholinesterase (BuChE) mutant.

XX KM Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KM butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.

XX OS Homo sapiens.
 OS Synthetic.

XX US6001625-A.
 XX 14-DEC-1999.
 XX 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 XX (USSA) US SEC OF ARMY.
 XX Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 XX Disclosure; Col 5-8; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 99.0%; Score 3228; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 4.4e-286;
 Matches 598; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGKGNLTVFGSTVAFIIGIP 60
 DB 1 MHSKVTITICIRFLFWFLILCMILIGKSHTEDDIIATKNGKRGKGNLTVFGSTVAFIIGIP 60
 QY 61 YAOPLGLRLRPFKKPOSITKMSDIWNATKYANSCCQNDQSPFGHSEMNPNPTDLSBDC 120
 DB 61 YAOPLGLRLRPFKKPOSITKMSDIWNATKYANSCCQNDQSPFGHSEMNPNPTDLSBDC 120
 QY 121 LYLNVWIPARKPKNAATVLIWIIYGGGFCOTGTSLSHVYDGKFLARVERVIVSMNRYVAGALG 180
 DB 121 LYLNVWIPARKPKNAATVLIWIIYGGGFCOTGTSLSHVYDGKFLARVERVIVSMNRYVAGALG 180
 QY 181 FLALPGNPEAPGNMGLFDQOLALQWVQKNTAAFGGNPKSVTLFGESAGAASVSHLLSPG 240
 DB 181 FLALPGNPEAPGNMGLFDQOLALQWVQKNTAAFGGNPKSVTLFGESAGAASVSHLLSPG 240
 QY 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPOEI 300
 DB 241 SHSLFTRAILIQQSGFNAPMAVTSIYEARNRTLNLAKLTGCSRENETEIIKCLRNKDPOEI 300
 QY 301 LLINEAFVVPYGTPLSVNPGFTVNDGFLTMDPDLLELGQFKKQIILVGNKDEGTWFLVY 360
 DB 301 LLINEAFVVPYGTPLSVNPGFTVNDGFLTMDPDLLELGQFKKQIILVGNKDEGTWFLVY 360
 QY 361 GAGPFSKDNNSITTRKEFOGLKIFPPGVSEFKESILFHTDWVDDQRPENYREALGDV 420
 DB 361 GAGPFSKDNNSITTRKEFOGLKIFPPGVSEFKESILFHTDWVDDQRPENYREALGDV 420
 QY 421 VGDYNIICPALFETKKESEKNNAPFYFFHRSSKLPPEMVGWGHYEIEFVGLPLER 480
 DB 421 VGDYNIICPALFETKKESEKNNAPFYFFHRSSKLPPEMVGWGHYEIEFVGLPLER 480

Db 421 VGDYNFICPALBETKFKFSEWGNNAFFYYFEHRSKLPMPBMGMVHGIEIEFVGLPLER 480
 QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNSTONNSTSWPVEKSTEOXYTLTNTSTRIMT 540
 Db 481 RDNVTKAEILSRISIVKRWANPAKYGNPNSTONNSTSWPVEKSTEOXYTLTNTSTRIMT 540
 QY 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
 Db 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
 QY 601 GL 602
 Db 601 GL 602
 RESULT 18
 AAY49486
 ID AAY49486 standard; protein; 602 AA.
 AC AAY49486;
 XX 27-MAR-2000 (first entry)
 DE Human butyryl cholinesterase (BuChE) mutant.
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KM butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX Homo sapiens.
 OS Synthetic.
 XX US6001625-A.
 PN 14-DEC-1999.
 PD 19-MAY-1995; 95US-00446100.
 PF 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 XX (USSA) US SEC OF ARMY.
 PA Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 DR Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 XX Disclosure; Col 11-12; 64pp; English.
 PS The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CAE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX Sequence 602 AA;
 SQ
 Query Match 99.0%; Score 3227; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 5.4e-286;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTIICIRFLFWELLICMLIGKSHTEDDIIITAKNGKVGAMLTIVGTVTAFLGIP 60
 Db 1 MDSKVTIICIRFLFWELLICMLIGKSHTEDDIIITAKNGKVGAMLTIVGTVTAFLGIP 60
 QY 61 YVAPPLGRLEFKKPGSLTMSDIWNAATKYANSCCONIDSPFGFHSEMANPNTDISEDC 120
 Db 61 YVAPPLGRLEFKKPGSLTMSDIWNAATKYANSCCONIDSPFGFHSEMANPNTDISEDC 120
 QY 121 LYANWIPAPKPKNAVLIMVIGGGQGTSSLAHYDGEFLARVRVTVVSNMYRGAIG 180
 Db 121 LYANWIPAPKPKNAVLIMVIGGGQGTSSLAHYDGEFLARVRVTVVSNMYRGAIG 180
 QY 181 FLALPGRPAPGNGMGLFDQOLALQWQKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
 Db 181 FLALPGRPAPGNGMGLFDQOLALQWQKNIAAFGNGPKSVTLFGESAGAASVSLHLSPG 240
 QY 241 SHSLFTRAILQSGSFNAVAVTSLYEARNRTNLAKLTGCSRENTEYIIKCLRNDPOBI 300
 Db 241 SHSLFTRAILQSGSFNAVAVTSLYEARNRTNLAKLTGCSRENTEYIIKCLRNDPOBI 300
 QY 301 LINEAFVVPYGPPLSVNPGPTVDGDLTMDPDLLELGOFKKTQILVGNKDEGTFLVY 360
 Db 301 LINEAFVVPYGPPLSVNPGPTVDGDLTMDPDLLELGOFKKTQILVGNKDEGTFLVY 360
 QY 361 GAPGFKDNNSITTRKEPQEGKIFPPGVSEFKESILPHYTDWDDORPENYREALGV 420
 Db 361 GAPGFKDNNSITTRKEPQEGKIFPPGVSEFKESILPHYTDWDDORPENYREALGV 420
 QY 421 VGDYNFICPALBETKFKFSEWGNNAFFYYFEHRSKLPMPBMGMVHGIEIEFVGLPLER 480
 Db 421 VGDYNFICPALBETKFKFSEWGNNAFFYYFEHRSKLPMPBMGMVHGIEIEFVGLPLER 480
 QY 481 RDNVTKAEILSRISIVKRWANPAKYGNPNSTONNSTSWPVEKSTEOXYTLTNTSTRIMT 540
 Db 481 RDNVTKAEILSRISIVKRWANPAKYGNPNSTONNSTSWPVEKSTEOXYTLTNTSTRIMT 540
 QY 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
 Db 541 KLRAGQCRFWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYTSKESCV 600
 QY 601 GL 602
 Db 601 GL 602
 RESULT 19
 AAY49485
 ID AAY49485 standard; protein; 602 AA.
 AC AAY49485;
 XX 27-MAR-2000 (first entry)
 DE Human butyryl cholinesterase (BuChE) mutant.
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KM butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX Homo sapiens.
 OS Synthetic.
 XX US6001625-A.
 PN 14-DEC-1999.
 PD 19-MAY-1995; 95US-00446100.
 PF 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 XX (USSA) US SEC OF ARMY.
 PA

PI Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 XX
 XX Disclosure; Col 9-12; 64pp; English.
 XX
 CC The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 SQ Sequence 602 AA;
 Query Match 99.0%; Score 3227; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 5.4e-286;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVAFGIP 60
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVAFGIP 60
 QY 61 YAOPPLGRLEPKKPOSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 DB 61 YAOPPLGRLEPKKPOSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 QY 121 LYANWVPAPKPKNAATVLIWYGGGFOTGSSLAHYDGKFLARVERIVVSMNRYVALG 180
 DB 121 LYANWVPAPKPKNAATVLIWYGGGFOTGSSLAHYDGKFLARVERIVVSMNRYVALG 180
 QY 181 FLALPGNEAPKNGGLPQOALQWQKNIAPGNGPKSVTLFPGSAGASVSLHLSPG 240
 DB 181 FLALPGNEAPKNGGLPQOALQWQKNIAPGNGPKSVTLFPGSAGASVSLHLSPG 240
 QY 241 SHSLFTTALIQSGSFNAPWATVSLYEARNRTLANLAKLTGCSRENETETIIKCLRNKDPEI 300
 DB 241 SHSLFTTALIQSGSFNAPWATVSLYEARNRTLANLAKLTGCSRENETETIIKCLRNKDPEI 300
 QY 301 LLAFAFVVPYGTPLSVNFGPTVDDFLTMDPDLLELGQFKKTOILVGNKDEGTWPLVY 360
 DB 301 LLAFAFVVPYGTPLSVNFGPTVDDFLTMDPDLLELGQFKKTOILVGNKDEGTWPLVY 360
 QY 361 GABGFSKDNNSIITRKEFOBELKIFPGVSEFGKESLILFHTDWDODRPNNYBALGDV 420
 DB 361 GABGFSKDNNSIITRKEFOBELKIFPGVSEFGKESLILFHTDWDODRPNNYBALGDV 420
 QY 421 VGDVNFICPALEFTTKTSEWGNNAFFYYFEHRSKLPWEMWGMHGEIEFVGLPLER 480
 DB 421 VGDVNFICPALEFTTKTSEWGNNAFFYYFEHRSKLPWEMWGMHGEIEFVGLPLER 480
 QY 481 RDNTYKABELLSRSIVKRWANPAKYGNPNTONNSTWPKSTBOXYLTANTESTRIMT 540
 DB 481 RDNTYKABELLSRSIVKRWANPAKYGNPNTONNSTWPKSTBOXYLTANTESTRIMT 540
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRNNNMMDKQNFNDYTSKKSCV 600
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDBAEWKAGFHRNNNMMDKQNFNDYTSKKSCV 600
 QY 601 GL 602

DB 601 GL 602
 RESULT 20
 ID AAY49488 standard; protein; 602 AA.
 AC AAY49488;
 XX
 XX 27-MAR-2000 (first entry)
 DT
 XX Human butyryl cholinesterase (BuChE) mutant.
 DE
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX
 XX Homo sapiens.
 OS Synthetic.
 PN US6001625-A.
 XX
 PD 14-DEC-1999.
 XX
 PF 19-MAY-1995; 95US-00446100.
 XX
 PR 19-MAY-1995; 95US-00446100.
 XX
 PA (USSA) US SEC OF ARMY.
 PI Broomfield CA, Lockridge O, Millard CB;
 XX WPI; 2000-096137/08.
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 XX
 XX Disclosure; Col 11-12; 64pp; English.
 XX
 CC The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 SQ Sequence 602 AA;
 Query Match 99.0%; Score 3227; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 5.4e-286;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVAFGIP 60
 DB 1 MHSKVTITICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGMNLTVFGGTVAFGIP 60
 QY 61 YAOPPLGRLEPKKPOSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 DB 61 YAOPPLGRLEPKKPOSLTKMSDIWMTKYANSCCONIDQSPFGHSEMMNPNTDLSDC 120
 QY 121 LYANWVPAPKPKNAATVLIWYGGGFOTGSSLAHYDGKFLARVERIVVSMNRYVALG 180

Db 121 LYINWIPAPKPKNAATVLWITGGGFGQTGTSLSHYTDGKFLARVERVIVSMNVGALG 180
 QY 181 FLALPGNEAPGNMGLFDQOLALQWOKNIAFAGNPKSVTLFGESAGAAVSILHLSFG 240
 Db 181 FLALPGNEAPGNMGLFDQOLALQWOKNIAFAGNPKSVTLFGESAGAAVSILHLSFG 240
 QY 241 SLSLFTRAIILOSGSFNAFPAVATSLYEARNRTNLAKLTCGSRNENETELIKCLRNKDPQEI 300
 Db 241 SLSLFTRAIILOSGSFNAFPAVATSLYEARNRTNLAKLTCGSRNENETELIKCLRNKDPQEI 300
 QY 301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQILVGNKDEGTWFLVY 360
 Db 301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQILVGNKDEGTWFLVY 360
 QY 361 GAPGFSKDNNSIITRKEFGELKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGV 420
 Db 361 GAPGFSKDNNSIITRKEFGELKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGV 420
 QY 421 VGDYNFICPALFETFKSEMGNNAFYYFPEHRSKLPWPMGVMGHEIEFVFGPLER 480
 Db 421 VGDYNFICPALFETFKSEMGNNAFYYFPEHRSKLPWPMGVMGHEIEFVFGPLER 480
 QY 481 RDNYTKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
 Db 481 RDNYTKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFRHNNYMDKNOFNDYTSKESCV 600
 Db 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFRHNNYMDKNOFNDYTSKESCV 600
 QY 601 GL 602
 Db 601 GL 602
 Db 601 GL 602
 RESULT 21
 AA49487
 ID AA49487 standard; protein; 602 AA.
 AC AA49487;
 DT 27-MAR-2000 (first entry)
 XX
 DE Human butyryl cholinesterase (BuChE) mutant.
 XX
 KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dlp; human;
 KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US6001625-A.
 PD 14-DEC-1999.
 PF 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 PA (USSA) US SEC OF ARMY.
 PI Broomfield CA, Lockridge O, Millard CB;
 DR WPI, 2000-096137/08.
 PT Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 PS Disclosure; Col 11-12; 64pp; English.
 CC The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterase (AChE),
 CC

CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weapons such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 CC
 XX
 SQ Sequence 602 AA;
 Query Match 99.0%; Score 3226; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 6.7e-286;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MSKVTIICIRPLFWFLICMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60
 Db 1 MSKVTIICIRPLFWFLICMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60
 QY 61 YAOPLGLRLFRKQPOSTLRKSDINWATRYANSCONIDQSPGTHGSEMNPNTDLSDC 120
 Db 61 YAOPLGLRLFRKQPOSTLRKSDINWATRYANSCONIDQSPGTHGSEMNPNTDLSDC 120
 QY 121 LYINWIPAPKPKNAATVLWITGGGFGQTGTSLSHYTDGKFLARVERVIVSMNVGALG 180
 Db 121 LYINWIPAPKPKNAATVLWITGGGFGQTGTSLSHYTDGKFLARVERVIVSMNVGALG 180
 QY 181 FLALPGNEAPGNMGLFDQOLALQWOKNIAFAGNPKSVTLFGESAGAAVSILHLSFG 240
 Db 181 FLALPGNEAPGNMGLFDQOLALQWOKNIAFAGNPKSVTLFGESAGAAVSILHLSFG 240
 QY 241 SLSLFTRAIILOSGSFNAFPAVATSLYEARNRTNLAKLTCGSRNENETELIKCLRNKDPQEI 300
 Db 241 SLSLFTRAIILOSGSFNAFPAVATSLYEARNRTNLAKLTCGSRNENETELIKCLRNKDPQEI 300
 QY 301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQILVGNKDEGTWFLVY 360
 Db 301 LINEAFVVPYGTPLSVNFGPTVDGDFLTMDPDLLELGQFKTQILVGNKDEGTWFLVY 360
 QY 361 GAPGFSKDNNSIITRKEFGELKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGV 420
 Db 361 GAPGFSKDNNSIITRKEFGELKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGV 420
 QY 421 VGDYNFICPALFETFKSEMGNNAFYYFPEHRSKLPWPMGVMGHEIEFVFGPLER 480
 Db 421 VGDYNFICPALFETFKSEMGNNAFYYFPEHRSKLPWPMGVMGHEIEFVFGPLER 480
 QY 481 RDNYTKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
 Db 481 RDNYTKAEILSRISIVKMANFAKYGNPNETONNSTMPVFKSTQKYLTLNTESTRIIMT 540
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFRHNNYMDKNOFNDYTSKESCV 600
 Db 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFRHNNYMDKNOFNDYTSKESCV 600
 QY 601 GL 602
 Db 601 GL 602
 Db 601 GL 602
 RESULT 22
 AA49482
 ID AA49482 standard; protein; 602 AA.
 AC AA49482;
 DT 27-MAR-2000 (first entry)

XX Human butyryl cholinesterase (BuChE) mutant.
 XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPA; mutant.
 XX Homo sapiens.
 OS Synthetic.
 PN US6001625-A.
 PD 14-DEC-1999.
 PF 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 PA (USSA) US SEC OF ARMY.
 PI Broomfield CA, Lockridge O, Millard CB;
 DR WPI; 2000-096137/08.
 PT Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 XX Disclosure; Col 9-10; 64pp; English.
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 XX Sequence 602 AA;
 SQ
 Query Match 98.9%; Score 3225; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 8.2e-286;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDSKVTIIICIRFLFWPLLCLMIGKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60
 DB 1 MHSKVTIIICIRFLFWPLLCLMIGKSHTEDDIIATKNGKVRGNLTVFGTVAFLGIP 60
 QY 61 YAOPLGLRLRKPKQSILTKSDIMNATKYANSCCONIDOSPFGHSEMMNPNDLSEDC 120
 DB 61 YAOPLGLRLRKPKQSILTKSDIMNATKYANSCCONIDOSPFGHSEMMNPNDLSEDC 120
 QY 121 LYLVNWIIPAPKPKNAATLWIIYGGAFOTGTSLSHVYOGKFLARVERVIVSMNRYVAGALG 180
 DB 121 LYLVNWIIPAPKPKNAATLWIIYGGAFOTGTSLSHVYOGKFLARVERVIVSMNRYVAGALG 180
 QY 181 FLALPGNPEAPNGNGLFDQOLALQWVQKNIAPFGSNPKSVTLFGESAGAAVSILHLSPG 240
 DB 181 FLALPGNPEAPNGNGLFDQOLALQWVQKNIAPFGSNPKSVTLFGESAGAAVSILHLSPG 240
 QY 241 SHSIFTRAILLOSGFNAPMNTSIVYKARNRLINAKLTGCRKRETEIKLRKNDQOEI 300
 DB 241 SHSIFTRAILLOSGFNAPMNTSIVYKARNRLINAKLTGCRKRETEIKLRKNDQOEI 300
 QY 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTDMDDILLELQGFKKQIILVGVNDEGTWFLVY 360

DB 301 LLINEAFVVPYGTPLSVNFGPTVDGDFLTDMDDILLELQGFKKQIILVGVNDEGTWFLVY 360
 QY 361 GARGFSKDNNSIITRKREFORGLKIPFGVSEFGKESILFFYTMVVDQRENTREALGDV 420
 DB 361 GARGFSKDNNSIITRKREFORGLKIPFGVSEFGKESILFFYTMVVDQRENTREALGDV 420
 QY 421 VGDYNFICPALIEFTKKESEWGNNAFFYYFEHRSSKLPWPEMGMVHGYSIEFVGLPLER 480
 DB 421 VGDYNFICPALIEFTKKESEWGNNAFFYYFEHRSSKLPWPEMGMVHGYSIEFVGLPLER 480
 QY 481 RDNVTKAEIILSRISIVKRWANPAKYGNDPNTONNSTSWPFKSTEQKYLTLNTESTIMT 540
 DB 481 RDNVTKAEIILSRISIVKRWANPAKYGNDPNTONNSTSWPFKSTEQKYLTLNTESTIMT 540
 QY 541 KLRAGQCRFTWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYSKKESSCV 600
 DB 541 KLRAGQCRFTWTSFPFKYLEMTGNIDEAEWEMKAGFHRMNNYMDMKQFNDYSKKESSCV 600
 QY 601 GL 602
 DB 601 GL 602
 RESULT 23
 ID AAY49481
 AA AAY49481 standard; protein; 602 AA.
 AC AAY49481;
 XX 27-MAR-2000 (first entry)
 XX Human butyryl cholinesterase (BuChE) mutant.
 DE Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KW butyrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
 KW nerve agent; organophosphorus acid anhydride; OPA; mutant.
 XX Homo sapiens.
 OS Synthetic.
 PN US6001625-A.
 PD 14-DEC-1999.
 PF 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 PA (USSA) US SEC OF ARMY.
 PI Broomfield CA, Lockridge O, Millard CB;
 DR WPI; 2000-096137/08.
 PT Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 XX Disclosure; Col 7-8; 64pp; English.
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE),
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human CaE). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with

CC Improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 98.9%; Score 3224; DB 3; Length 602;

Best Local Similarity 99.3%; Pred. No. 1e-285; Mismatches 4; Indels 0; Gaps 0;

Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTITICRFLFWFLILCMILGKSTEDDIIATKNGKVRGMNLTVFGTATATLGP 60
 DB 1 MHSKVTITICRFLFWFLILCMILGKSTEDDIIATKNGKVRGMNLTVFGTATATLGP 60
 QY YAOPLGLRLFRKPGQSLTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPVTLSEDC 120
 DB YAOPLGLRLFRKPGQSLTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPVTLSEDC 120
 QY 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERIVVSMNYRVGALG 180
 DB 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERIVVSMNYRVGALG 180
 QY 181 FLALPGNPEAPGNMGFLDQQLALQWQKNTAAFGGNPKSVTLFGESAGAAVSILHLSPG 240
 DB 181 FLALPGNPEAPGNMGFLDQQLALQWQKNTAAFGGNPKSVTLFGESAGAAVSILHLSPG 240
 QY 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKPOEI 300
 DB 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKPOEI 300
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTMEDPILILEGQFKTQIIVGVNKDEGTWFLVY 360
 DB 301 LNEAFVVPYGTPLSVNFGPTVDGFLTMEDPILILEGQFKTQIIVGVNKDEGTWFLVY 360
 QY 361 GABPFSKDNNSITTRKPFQEGELKIFPGVSEFGKESILFHYTWDVDDQRENREALGDV 420
 DB 361 GABPFSKDNNSITTRKPFQEGELKIFPGVSEFGKESILFHYTWDVDDQRENREALGDV 420
 QY 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVGMGEIEIEFVGLPLER 480
 DB 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVGMGEIEIEFVGLPLER 480
 QY 481 RDNVTKAEELISRSIVKMANFAKYNPNETONNSTMPVFKSTQKYLTLNTESTRIMT 540
 DB 481 RDNVTKAEELISRSIVKMANFAKYNPNETONNSTMPVFKSTQKYLTLNTESTRIMT 540
 QY 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRNNYMMQKQFNDYTSKESCV 600
 DB 541 KLRAGQCRFWTSFPPKYLEMTGNIDEAEWEKAGFHRNNYMMQKQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 24

AA49480 ID AA49480 standard; protein; 602 AA.

XX AA49480;

XX 27-MAR-2000 (first entry)

XX Human butyryl cholinesterase (Buche) mutant.

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;

XX butyrylcholinesterase; Buche; carboxylesterase; Gae; sheep dip; human;

XX nerve agent; organophosphorus acid anhydride; OPAA; mutant.

XX Homo sapiens.

XX Synthetic.

XX US6001625-A.

XX 14-DEC-1999.
 XX 19-MAY-1995; 95US-00446100.
 XX 19-MAY-1995; 95US-00446100.
 XX (USSA) US SEC OF ARMY.
 XX Broomfield CA, Lockridge O, Millard CB;
 XX WPI, 2000-096137/08.
 XX Enhancing the organophosphate detoxifying capabilities of esterases for
 XX the treatment of organophosphate poisoning.
 XX Disclosure; Col 7-8; 64pp; English.

CC The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (Buche) and/or carboxylesterases (Gae)), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human Buche and/or human Gae). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match 98.9%; Score 3223; DB 3; Length 602;

Best Local Similarity 99.3%; Pred. No. 1.3e-285; Mismatches 4; Indels 0; Gaps 0;

Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTITICRFLFWFLILCMILGKSTEDDIIATKNGKVRGMNLTVFGTATATLGP 60
 DB 1 MHSKVTITICRFLFWFLILCMILGKSTEDDIIATKNGKVRGMNLTVFGTATATLGP 60
 QY YAOPLGLRLFRKPGQSLTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPVTLSEDC 120
 DB YAOPLGLRLFRKPGQSLTKMSDIWNAATKYANSCCONIDSPFGHSEMMNPVTLSEDC 120
 QY 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERIVVSMNYRVGALG 180
 DB 121 LYNWVWPAPKPKNAATVLIWYGGGFQGTSSLHVYDGKFLARVERIVVSMNYRVGALG 180
 QY 181 FLALPGNPEAPGNMGFLDQQLALQWQKNTAAFGGNPKSVTLFGESAGAAVSILHLSPG 240
 DB 181 FLALPGNPEAPGNMGFLDQQLALQWQKNTAAFGGNPKSVTLFGESAGAAVSILHLSPG 240
 QY 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKPOEI 300
 DB 241 SHSLFTRAILIQQSGSFNAPMAVTSLYEARNRTLNAKLTCGSRNETEIIKCLRNKPOEI 300
 QY 301 LNEAFVVPYGTPLSVNFGPTVDGFLTMEDPILILEGQFKTQIIVGVNKDEGTWFLVY 360
 DB 301 LNEAFVVPYGTPLSVNFGPTVDGFLTMEDPILILEGQFKTQIIVGVNKDEGTWFLVY 360
 QY 361 GABPFSKDNNSITTRKPFQEGELKIFPGVSEFGKESILFHYTWDVDDQRENREALGDV 420
 DB 361 GABPFSKDNNSITTRKPFQEGELKIFPGVSEFGKESILFHYTWDVDDQRENREALGDV 420
 QY 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVGMGEIEIEFVGLPLER 480
 DB 421 VGDYNFICPALFETKFSSEMNNAFFYYFHRSSKLPMPBMGMVGMGEIEIEFVGLPLER 480

QY 481 RDNTKAEILSRISIVKMANPAKYGNPNETONNSTSWPKSTEOKYLTLNTESTRIIMT 540
 DB 481 RDNTKAEILSRISIVKMANPAKYGNPNETONNSTSWPKSTEOKYLTLNTESTRIIMT 540
 QY 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600
 DB 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

RESULT 25
 AAY49479
 ID AAY49479 standard; protein; 602 AA.
 AC AAY49479;
 XX 27-MAR-2000 (first entry)
 DE Human butyryl cholinesterase (BuChE) mutant.
 KM Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KM butyrylcholinesterase; BuChE; carboxylesterase; Cab; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPAA; mutant.
 OS Homo sapiens.
 OS Synthetic.
 XX US6001625-A.
 PN 14-DEC-1999.
 PD 19-MAY-1995; 95US-00446100.
 PR 19-MAY-1995; 95US-00446100.
 XX (USSA) US SEC OF ARMY.
 PA Broomfield CA, Lockridge O, Millard CB;
 PI WPI; 2000-096137/08.
 DR Enhancing the organophosphate detoxifying capabilities of esterases for
 PT the treatment of organophosphate poisoning.
 XX Disclosure; Col 7-8; 64pp; English.
 XX The invention provides a method of enhancing organophosphate detoxifying
 CC capabilities of esterases (either human acetylcholinesterases (AChE), that
 CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (Cab), that
 CC comprises substituting a histidine residue for 1 or more amino acid(s)
 CC within 6 Angstrom of an active site serine. The method may be used for
 CC enhancing organophosphate detoxifying capabilities of esterases (either
 CC human AChE, human BuChE and/or human Cab). The modified esterases may
 CC then be used to treat agricultural workers poisoned with organophosphates
 CC through contact with chemical such as sheep dips. They may also be used
 CC to treat military personnel contaminated by chemical weaponry such as
 CC nerve agents. Additionally, the esterases may also be used to
 CC decontaminate ground and buildings and equipment used to store, or
 CC contaminated by organophosphates. The method produces esterases with
 CC improved detoxification properties over naturally occurring
 CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
 CC less likely to be inactivated by the OPAA
 XX
 SQ Sequence 602 AA;

Query Match 98.9%; Score 323; DB 3; Length 602;
 Best Local Similarity 99.3%; Pred. No. 1.3e-285;
 Matches 598; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60

DB 1 MDSKVTIICIRFLFWFLLCMLIGKSHTEDDIIATKNGKVRGNLTVFGGTVAFLGIP 60
 QY YAOPLGRLEAFKPOSITKMSDIWNAATKYNSSCONIDQSFPGPHSEMNPNTDISEDC 120
 DB 61 YAOPLGRLEAFKPOSITKMSDIWNAATKYNSSCONIDQSFPGPHSEMNPNTDISEDC 120
 QY LYLNWMIAPKPKNAATVLIWYGGGFGTGTSSLHVYDGKFLARVERIVVSMYRVGALG 180
 DB LYLNWMIAPKPKNAATVLIWYGGGFGTGTSSLHVYDGKFLARVERIVVSMYRVGALG 180
 QY FLALPGNPEAPGNWGLFDQOLALQWOKNTAAAGGNPKSYTLFGESAGAAVSLSHLSPG 240
 DB FLALPGNPEAPGNWGLFDQOLALQWOKNTAAAGGNPKSYTLFGESAGAAVSLSHLSPG 240
 QY SHSLFTRALIOSGSPNAPMAVTSIYEARNRTLMLAKLTGCSRENETIICLRNKDPOEI 300
 DB SHSLFTRALIOSGSPNAPMAVTSIYEARNRTLMLAKLTGCSRENETIICLRNKDPOEI 300
 QY LLINEAFVVPYGTPLSVNFGPTVDGDFLTDPDILLBLGQFKTQILVGNKDEGTWFLVY 360
 DB LLINEAFVVPYGTPLSVNFGPTVDGDFLTDPDILLBLGQFKTQILVGNKDEGTWFLVY 360
 QY GARGFSKONNSITTRKEFGGLKIFPPGVSEFGKESILFHYTWWDQRENTREALGDV 420
 DB GARGFSKONNSITTRKEFGGLKIFPPGVSEFGKESILFHYTWWDQRENTREALGDV 420
 QY VGDYNFICPALFETKKSEWGNNAFFYYFEHRSSKLPMPMGVMHGYEIEFVGLPLER 480
 DB VGDYNFICPALFETKKSEWGNNAFFYYFEHRSSKLPMPMGVMHGYEIEFVGLPLER 480
 QY 481 RDNTKAEILSRISIVKMANPAKYGNPNETONNSTSWPKSTEOKYLTLNTESTRIIMT 540
 DB 481 RDNTKAEILSRISIVKMANPAKYGNPNETONNSTSWPKSTEOKYLTLNTESTRIIMT 540
 QY 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600
 DB 541 KLRNQCRFWTSFPPKYLEMTGNIDEAEWEMKAGFHRMNNYMDWKQFNDYTSKESCV 600
 QY 601 GL 602
 DB 601 GL 602

Search completed: January 6, 2005, 09:37:30
 Job time : 165 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:42:34 ; Search time 197 Seconds

(without alignments)
1676.472 Million cell updates/sec

Title: US-09-748-739a-2_COPY_29_602

Perfect score: 3110
Sequence: 1 EDDIIITAKNGKVRGNMLTV.....MDWKNGPDYTSKSCVGL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3096	99.5	602	1	CHLE_HUMAN
2	2843	91.4	581	1	CHLE_RABIT
3	2775	89.2	602	2	OGNIN9
4	2774	89.2	574	1	CHLE_HORSE
5	2696	86.7	602	1	CHLE_FELICA
6	2684	86.3	603	1	CHLE_PANTT
7	2530.	81.4	603	2	BAC31196
8	2521	81.1	603	1	CHLE_MOUSE
9	2505	80.5	597	2	OGJFC1
10	2289	73.6	603	2	O90ZK8
11	1765.5	56.8	634	1	ACES_BRARE
12	1765	56.8	633	1	ACES_ELEBL
13	1722.5	55.4	606	1	ACES_BUNFA
14	1689	54.3	614	1	ACES_HUMAN
15	1689	54.3	614	2	AAP23365
16	1678.5	54.0	614	1	ACES_RAT
17	1675.5	53.9	614	1	ACES_MOUSE
18	1675.5	53.9	614	2	BAC31228
19	1675.5	53.9	614	2	BAC31641
20	1675.5	53.9	614	2	BAC32595
21	1674	53.8	349	2	O9GKJ6
22	1666.5	53.6	611	1	ACES_FELICA
23	1663.5	53.5	613	1	ACES_BOVIN
24	1649.5	53.0	584	1	ACES_RABIT
25	1649	53.0	590	1	ACES_TORNA
26	1648	53.0	586	1	ACES_TORCA
27	1557.5	50.1	617	2	OG6TM9
28	1455.5	46.8	767	1	ACES_CHICK
29	1435	46.1	602	2	O76959
30	1376	44.2	605	2	O76998
31	1358	43.7	526	2	O86YX9

32	1323	42.5	701	2	O75VX9	O75VX9	culex trita
33	1323	42.5	701	2	BAD06210	BAD06210	culex trita
34	1317	42.3	702	1	ACES_CULPI	ACES_CULPI	culex pipie
35	1302	41.9	623	1	O7RTM0	O7RTM0	anopheles g
36	1302	41.9	737	1	ACES_ANOGA	ACES_ANOGA	anopheles g
37	1302	41.9	743	2	O7PUE2	O7PUE2	anopheles g
38	1294	41.6	559	2	O7PKM1	O7PKM1	anopheles g
39	1273	40.9	687	2	O86C24	O86C24	tetranychus
40	1220	39.2	676	2	O9BMJ1	O9BMJ1	schizaphis
41	1216	39.1	660	2	O6KAV3	O6KAV3	aphis gossy
42	1213	39.0	671	2	O6KAV4	O6KAV4	aphis gossy
43	1212	39.0	676	2	O8MW35	O8MW35	aphis gossy
44	1209	38.9	675	2	O6KAV5	O6KAV5	aphis gossy
45	1195	38.4	610	2	O9J110	O9J110	Opal
46	1177.5	37.9	677	2	O9NTH6	O9NTH6	nephroetix
47	1172	37.7	656	2	O96529	O96529	meloidogyne
48	1166	37.5	656	2	O9YXA9	O9YXA9	meloidogyne
49	1146	36.8	638	2	O86OW5	O86OW5	helicoverpa
50	1145	36.8	620	1	ACES_CABER	ACES_CABER	caenorhabdi
51	1143	36.8	647	2	O8MX85	O8MX85	helicoverpa
52	1142	36.7	620	1	ACES_CABEL	ACES_CABEL	caenorhabdi
53	1135	36.5	629	1	ACES_LEPDE	ACES_LEPDE	leptinotars
54	1129	36.3	638	2	O8MZL2	O8MZL2	plutella xy
55	1127	36.2	585	2	O7RTL6	O7RTL6	clona intes
56	1088.5	35.0	550	2	O7RTL7	O7RTL7	clona intes
57	1079	34.7	587	2	O6XR74	O6XR74	rhhipicephal
58	1079	34.7	587	2	AAP49302	AAP49302	rhhipicephal
59	1079	34.7	593	2	O6XR75	O6XR75	rhhipicephal
60	1079	34.7	593	2	AAP49301	AAP49301	rhhipicephal
61	1073	34.5	590	2	O61987	O61987	boophilus d
62	1070.5	34.4	637	2	O9TX11	O9TX11	aedes aegypt
63	1065	34.2	596	2	O6XR73	O6XR73	dermaceror
64	1065	34.2	596	2	AAP49303	AAP49303	dermaceror
65	1063.5	34.2	645	2	O70FG0	O70FG0	anopheles g
66	1063.5	34.2	645	2	O7RTL9	O7RTL9	anopheles g
67	1059.5	34.1	664	1	ACES_ANOST	ACES_ANOST	anopheles s
68	1055.5	33.9	633	2	O75VY0	O75VY0	culex trita
69	1055.5	33.9	633	2	BAD06209	BAD06209	culex trita
70	1045.5	33.6	692	2	O95P20	O95P20	musca domes
71	1045.5	33.6	692	2	O95WV7	O95WV7	musca domes
72	1045	33.6	595	2	O45210	O45210	boophilus m
73	1044	33.6	649	1	ACES_DROME	ACES_DROME	drosophila
74	1043.5	33.6	692	2	O8MXC6	O8MXC6	musca domes
75	1043.5	33.6	692	2	O8MXC8	O8MXC8	musca domes
76	1043.5	33.6	692	2	O8MXC9	O8MXC9	musca domes
77	1042.5	33.5	610	2	O7YZP7	O7YZP7	trialeurode
78	1040.5	33.5	692	2	O8MXC4	O8MXC4	musca domes
79	1038.5	33.4	612	2	O8MW09	O8MW09	musca domes
80	1037.5	33.4	691	2	O8MXC5	O8MXC5	musca domes
81	1036.5	33.3	692	2	O8MXC7	O8MXC7	musca domes
82	1033.5	33.2	664	2	O8RTU9	O8RTU9	musca domes
83	1029.5	33.1	708	2	P91954	P91954	lucilia cup
84	1028.5	33.1	692	2	O7YU9	O7YU9	musca domes
85	1027.5	33.0	673	2	O8MW24	O8MW24	bactrocera
86	1024.5	32.9	603	2	O7YZC0	O7YZC0	myzus persi
87	1019.5	32.8	528	2	O62563	O62563	rhhipicephal
88	1019.5	32.8	604	1	ACES_CABER	ACES_CABER	caenorhabdi
89	1014.5	32.6	338	1	ACES_MYXGL	ACES_MYXGL	caenorhabdi
90	1013	32.6	664	2	O8WV36	O8WV36	aphis gossy
91	1012.5	32.6	602	2	O61372	O61372	caenorhabdi
92	1008	32.4	461	2	O7YZP8	O7YZP8	bemisia tab
93	959	30.8	492	2	O9GQP7	O9GQP7	aple mellif
94	957	30.8	615	2	O86GL7	O86GL7	dicyocaulu
95	954	30.7	512	2	O8WZM0	O8WZM0	plutella xy
96	948	30.5	629	2	O61371	O61371	caenorhabdi
97	946	30.4	629	2	O61378	O61378	caenorhabdi
98	944	30.4	592	2	O6QDP4	O6QDP4	dicyocaulu
99	944	30.4	592	2	AAS49411	AAS49411	dicyocaulu
100	943	30.3	604	2	O9NDG9	O9NDG9	caenorhabdi

ALIGNMENTS

RESULT 1

ID	CHLE_HUMAN	STANDARD;	PRT;	602 AA.
AC	06276;			
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-AUG-1988	(Rel. 08, Last sequence update)		
DT	01-OCT-2004	(Rel. 45, Last annotation update)		
DE	Cholinesterase precursor (EC 3.1.1.8) (acetylcholine acetylcholinesterase)			
DE	(Choline esterase II) (Butyrylcholine esterase)			
DE	(Pseudocholinesterase).			
DE	Name=BCHE; Synonyms=CHE1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Butheraia; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90212557; PubMed=2322535;			
RA	Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,			
RA	Lockridge O.,			
RT	"Structure of the gene for human butyrylcholinesterase. Evidence for a			
RT	single copy."			
RT	Biochemistry 29:124-131(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal;			
RX	MEDLINE=87231856; PubMed=3035536;			
RA	Prody C.A., Zevin-Sonkin D., Gnat A., Goldberg O., Soreg H.,			
RT	"Isolation and characterization of full-length cDNA clones coding for			
RT	cholinesterase from fetal human tissues."			
RT	Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=88016155; PubMed=3477799;			
RA	Wetlieman C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,			
RA	Kott M., Rosenberry T.L., la Du B.N., Lockridge O.,			
RT	"Brain cDNA clone for human cholinesterase."			
RT	Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Zollner F.S., Wagner L., Shennan C.M., Schler G.D.,			
RA	Altshuler S.F., Zeelberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsien F.,			
RA	Datchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,			
RA	Bromstein M.J., Udell T.B., Tohyuki S., Carninci P., Mullaly S.J.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McLean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Valliant D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smalins D.E.,			
RA	Schmehk A., Schein J.E., Jones S.J.W., Maira M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[5]			
RP	SEQUENCE OF 29-602.			
RC	TISSUE=Plasma;			
RX	MEDLINE=87109144; PubMed=3542989;			
RA	Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,			
RA	Johnson L.L.,			
RT	"Complete amino acid sequence of human serum cholinesterase."			
RT	J. Biol. Chem. 262:549-557(1987).			
RN	[6]			

[illegible]

Db 449 EHRSSKLPWEMMGVMEHYIEEVEFGLPERDNYTKAEELISRSIVKRWANFAKYNP 508

Qy 481 NETQNMSTSNWFEVFEKTYITLTTESTRINTTKRAQOCRWTSFPFVLEMTGNIDAE 540

Db 509 NETQNMSTSNWFEVFEKTYITLTTESTRINTTKRAQOCRWTSFPFVLEMTGNIDAE 568

Qy 541 WEMKAGFPRNNYMMDMKQFNPDYTSKSKSCVGL 574

Db 569 WEMKAGFPRNNYMMDMKQFNPDYTSKSKSCVGL 602

RESULT 2

CHLE_RABIT STANDARD; PRT: 581 AA.

AC P21927; 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)

DE (Choline esterase II) (Butyrylcholine esterase)

DE (Pseudocholinesterase).

GN Name=BCH2;

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

KN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=New Zealand;

RX MEDLINE=90326526; PubMed=2374720;

RA Thilo O., Roudant S., Chatonnet A.,

RT "Complete sequence of rabbit butyrylcholinesterase.";

RL Nucleic Acids Res. 18:3990-3990(1990).

RN [2]

RP SEQUENCE OF 75-215 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=91201348; PubMed=2016308;

RA Arragaus M., Chatonnet A., Maasson P., Newton M., Vaughan T.A.,

RA Battells C.F., Nogueira C.P., La Du B.N., Lockridge O.,

RT "Use of the polymerase chain reaction for homology probing of

RL butyrylcholinesterase from several vertebrates.";

RL J. Biol. Chem. 266:6966-6974(1991).

CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a

CC carboxylic acid anion.

CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The

CC two subunits in a dimer are linked by a disulfide bond.

CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.

CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with

CC organophosphate esters.

CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X52090; CAA36308.1; -

DR EMBL; X52091; CAA36308.1; JOINED.

DR EMBL; X52092; CAA36308.1; JOINED.

DR EMBL; M62179; AAA31169.1; -

DR PIR; S10255; C39768.

DR HSSP; P22303; IFRU.

DR InterPro; IPR002019; CarbesteraseB.

DR InterPro; IPR000997; Cholinesterase.

DR InterPro; IPR000379; Ser_estr.

DR Pfam; PF00135; Coesterase; 1.

DR PRINTS; PR00878; Coesterase; 1.

DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

DR GlycoProtein; Hydrolase; Serine esterase; Signal.

FT SIGNAL 1 8 Potential.
FT CHAIN 9 581 Cholinesterase.
FT ACT SITE 205 205 Acyl-ester intermediate (By similarity).
FT ACT_SITE 332 332 Charge relay system (By similarity).
FT ACT_SITE 445 445 Charge relay system (By similarity).
FT DISULFID 72 99 By similarity.
FT DISULFID 259 270 By similarity.
FT DISULFID 407 526 By similarity.
FT DISULFID 578 578 Interchain (By similarity).
FT CARBOHYD 113 64 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 248 248 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 263 263 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 348 348 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 462 462 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 493 493 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 581 AA; 66156 MW; PE8B199E7B32EBA CRC64;

Query Match 91.4%; Score 2843; DB 1; Length 581;
Best Local Similarity 92.0%; Pred. No. 2,4e-205;
Matches 526; Conservative 12; Mismatches 34; Indels 0; Gaps 0;

QY 2 DDIIATKNGKRGVNLTVFGVTAFLGIPYAPPLGRLFFKKQSLTKMSDIMNATKY 61
DB 9 EDVITITKNGKRGVNLTVFGVTAFLGIPYAPPLGRLFFKKQSLTKMSDIMNATKY 68
QY 62 ANSCCONIDQSPFGHSEMMNPNTDISEDLTYNWMIPAKPKNAATVLMWYGGGFOTG 121
DB 69 ANSCCONIDQSPFGHSEMMNPNTDISEDLTYNWMIPAKPKNAATVLMWYGGGFOTG 128
QY 122 TSSLHVYDGKFLARVERIVVSMYRVAGLFLALPGNPEAPGMGLFDQGLALQWQK 181
DB 129 TSSLHVYDGKFLARVERIVVSMYRVAGLFLALPGNPEAPGMGLFDQGLALQWQK 188
QY 182 IAAFGNGKSVTLFESAGAAVSLSHLSPSGSHLFTRAIIQSSGSPNAPMAVTSLEYARN 241
DB 189 IAAFGNGKSVTLFESAGAAVSLSHLSPSGSHLFTRAIIQSSGSPNAPMAVTSLEYARN 248
QY 242 RTLANAKLTGCSRENETEIIKCLRNDPOEILINEAFVVPYGTPLSVNFGFTVGDPLTD 301
DB 249 RTLANAKLTGCSRENETEIIKCLRNDPOEILINEAFVVPYGTPLSVNFGFTVGDPLTD 308
QY 302 MPDILLEIQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSITRKKEFOGLKIFPPGV 361
DB 309 MPDILLEIQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSITRKKEFOGLKIFPPGV 368
QY 362 SRFGEKSLIFHTYDWDORPENYREALGDVVDGNFICPALEFKKSEMGNNAFYYF 421
DB 369 SRFGEKSLIFHTYDWDORPENYREALGDVVDGNFICPALEFKKSEMGNNAFYYF 428
QY 422 EHRSSKLPWPEWNGVHGIEIFVGLPLERRDNTYKAEIISRSIVKMANFAYKGNP 481
DB 429 EHRSSKLPWPEWNGVHGIEIFVGLPLERRDNTYKAEIISRSIVKMANFAYKGNP 488
QY 482 EYONNSTSPVPKSTQKYLINTESTRIIMTKLRAQQCFWTSFPPKYLEMTGNIDAEW 541
DB 489 EYONNSTSPVPKSTQKYLINTESTRIIMTKLRAQQCFWTSFPPKYLEMTGNIDAEW 548
QY 542 EWKAGFHRNNYMMDKQNFNDYTSKESCVG 573
DB 549 EWKAGFHRNNYMMDKQNFNDYTSKESCVG 580

RESULT 3
Q9N1N9 PRELIMINARY; PRT; 602 AA.
AC Q9N1N9 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase (EC 3.1.1.8).

GN Name=BCHE;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20181263; PubMed=10718335;
RA Wierdl M., Morton C.L., Danks M.K., Potter P.M.,
RT "Isolation and characterization of a cDNA encoding a horse liver
butyrylcholinesterase: evidence for CPT-11 drug activation."
RL Biochem. Pharmacol. 59:773-781 (2000).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AF178685; AAF61480.1; -.
DR HSSP; P21836; INSM.
DR GO; GO:0004104; F:cholinesterase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR003379; Ser. ester.
DR Pfam; PF00878; Cholinesterase; 1.
DR PRINTS; PR00878; Cholinesterase.
DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR Hydrolase.
SQ SEQUENCE 602 AA; 68838 MW; 94C73F00431DF26E CRC64;

Query Match 89.2%; Score 2775; DB 2; Length 602;
Best Local Similarity 90.7%; Pred. No. 3,4e-200;
Matches 518; Conservative 19; Mismatches 34; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKRGVNLTVFGVTAFLGIPYAPPLGRLFFKKQSLTKMSDIMNATKY 60
DB 29 EDDIIATKNGKRGVNLTVFGVTAFLGIPYAPPLGRLFFKKQSLTKMSDIMNATKY 88
QY 61 YANSCCONIDQSPFGHSEMMNPNTDISEDLTYNWMIPAKPKNAATVLMWYGGGFOT 120
DB 89 YANSCCONIDQSPFGHSEMMNPNTDISEDLTYNWMIPAKPKNAATVLMWYGGGFOT 148
QY 121 GTSLSHVYDGKFLARVERIVVSMYRVAGLFLALPGNPEAPGMGLFDQGLALQWQK 180
DB 149 GTSLSHVYDGKFLARVERIVVSMYRVAGLFLALPGNPEAPGMGLFDQGLALQWQK 208
QY 181 NIAAFNGKPSVTLFESAGAAVSLSHLSPSGSHLFTRAIIQSSGSPNAPMAVTSLEYARN 240
DB 209 NIAAFNGKPSVTLFESAGAAVSLSHLSPSGSHLFTRAIIQSSGSPNAPMAVTSLEYARN 268
QY 241 NRTLANAKLTGCSRENETEIIKCLRNDPOEILINEAFVVPYGTPLSVNFGFTVGDPLTD 300
DB 269 NRTLANAKLTGCSRENETEIIKCLRNDPOEILINEAFVVPYGTPLSVNFGFTVGDPLTD 328
QY 301 DMPDILLEIQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSITRKKEFOGLKIFPPGV 360
DB 329 DMPDILLEIQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSITRKKEFOGLKIFPPGV 388
QY 361 VSEFGEKSLIFHTYDWDORPENYREALGDVVDGNFICPALEFKKSEMGNNAFYYF 420
DB 389 VSEFGEKSLIFHTYDWDORPENYREALGDVVDGNFICPALEFKKSEMGNNAFYYF 448
QY 421 FEHRSSKLPWPEWNGVHGIEIFVGLPLERRDNTYKAEIISRSIVKMANFAYKGNP 480
DB 449 FEHRSSKLPWPEWNGVHGIEIFVGLPLERRDNTYKAEIISRSIVKMANFAYKGNP 508
QY 481 NETONNSTSPVPKSTQKYLINTESTRIIMTKLRAQQCFWTSFPPKYLEMTGNIDAEW 540
DB 509 NETONNSTSPVPKSTQKYLINTESTRIIMTKLRAQQCFWTSFPPKYLEMTGNIDAEW 568
QY 541 EWKAGFHRNNYMMDKQNFNDYTSKESCVG 571
DB 569 EWKAGFHRNNYMMDKQNFNDYTSKESCVG 599

RESULT 4

CHLE_HORSE
ID CHLE_HORSE STANDARD; PRT; 574 AA.
AC P81908;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EQ-
BCH).

GN Name=BCH;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA Moored D.R., Luo C., Garcia G.E., Doctor B.P.;
RT "Amino acid sequence of horse serum butyrylcholinesterase."
RL (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.
(eds.);
RL Structure and function of cholinesterases and related proteins,
RL pp.145-146, Plenum Press, New York and London (1998).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR HSBP; P21836; INSM.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine esterase.
FT ACT_SITE 198 198 Acyl-ester intermediate (By similarity).
FT ACT_SITE 325 325 Charge relay system (By similarity).
FT ACT_SITE 438 438 Charge relay system (By similarity).
FT DISULFID 65 92 By similarity.
FT DISULFID 252 263 By similarity.
FT DISULFID 400 519 By similarity.
FT DISULFID 571 571 Interchain (By similarity).
FT CARBOHYD 57 57 N-linked (G1CNAc...)
FT CARBOHYD 106 106 N-linked (G1CNAc...)
FT CARBOHYD 241 241 N-linked (G1CNAc...)
FT CARBOHYD 256 256 N-linked (G1CNAc...)
FT CARBOHYD 341 341 N-linked (G1CNAc...)
FT CARBOHYD 455 455 N-linked (G1CNAc...)
FT CARBOHYD 481 481 N-linked (G1CNAc...)
FT CARBOHYD 486 486 N-linked (G1CNAc...)
SQ SEQUENCE 574 AA; 65641 MW; 07755EB9FB9CB33E CMC64;
Query Match 89.2%; Score 2774; DB 1; Length 574;
Best Local Similarity 90.5%; Pred. No. 3.8e-200;
Matches 517; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 181 NIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILDGGSPNAPWATSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILDGGSPNAPWATSLYEAR 240
QY 241 NRTLNIAKLGCGRNTEIILKLRNMDPOEILINFAVVPYGPPLSVNPGPTVDDGFLT 300
DB 241 NRTLNIAKLGCGRNTEIILKLRNMDPOEILINFAVVPYGPPLSVNPGPTVDDGFLT 300
QY 301 DMPDILLEGQFKKTLIVGNKDEGTWFLVYGAPGSKDNNSIITKEPQEGIKTFPPG 360
DB 301 DMPDILLEGQFKKTLIVGNKDEGTWFLVYGAPGSKDNNSIITKEPQEGIKTFPPG 360
QY 361 VSEFGKESILFHYTDVDDGPENYRBDGVDVYDFICPALFETKESKGNNAFFY 420
DB 361 VSEFGKESILFHYTDVDDGPENYRBDGVDVYDFICPALFETKESKGNNAFFY 420
QY 421 FEHRSSKLPPEWGWVGHGIEFVRLPLERRDNTKAEIISRSIVKRNAPAKYGNP 480
DB 421 FEHRSSKLPPEWGWVGHGIEFVRLPLERRDNTKAEIISRSIVKRNAPAKYGNP 480
QY 481 NETQNSTSWPVPKSTQKTLTNTSESTRIMTKLRQAQCFMTSPFKVLEMTGNDIEAE 540
DB 481 NETQNSTSWPVPKSTQKTLTNTSESTRIMTKLRQAQCFMTSPFKVLEMTGNDIEAE 540
QY 541 MEWKAGFHRNNYMMDKQNFNDYTSKESK 571
DB 541 MEWKAGFHRNNYMMDKQNFNDYTSKESK 571

RESULT 5

CHLE_FELCA
ID CHLE_FELCA STANDARD; PRT; 602 AA.
AC 062760;
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCH;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RA MEDLINE=20334351; PubMed=10874122;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma."
RL Biochem. Pharmacol. 60:479-487(2000).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond (By
CC similarity).
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters (By similarity).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
DR HSBP; AF053483; AAC06261.1; -
DR HSBP; P22303; 1B41.

DR InterPro: IPR002018; CarboxylesteraseB.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estr.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR GlycoProtein: Hydrolase; Serine esterase; Signal.
 KW SIGNAL
 FT CHAIN 1
 FT ACT_SITE 29 602
 FT ACT_SITE 226 226
 FT ACT_SITE 353 353
 FT ACT_SITE 466 466
 FT DISULFID 93 120
 FT DISULFID 280 291
 FT DISULFID 428 547
 FT DISULFID 599 599
 FT CARBOHYD 85 85
 FT CARBOHYD 134 134
 FT CARBOHYD 269 269
 FT CARBOHYD 284 284
 FT CARBOHYD 369 369
 FT CARBOHYD 483 483
 FT CARBOHYD 509 509
 FT CARBOHYD 513 513
 FT CARBOHYD 514 514
 FT CARBOHYD 514 514
 FT SEQUENCE 602 AA; 68328 MW; ECB8879232B74B9C CRC64;

Query Match 86.7%; Score 2696; DB 1; Length 602;
 Best Local Similarity 87.6%; Pred. No. 3e-194;
 Matches 503; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

QY 1 EDDITAKKKNKVMNLTGPGTATLGIPIVAPOPGRGRFKPKKOSLTKMSIMNATK 60
 DB 29 BEDITTTKNGKVRKMNPLVDGYTATLGIPIVAPOPGRGRFKPKKOSLTKMSIMNATK 88
 QY 61 YANSCQNIIDSPFGHSEMMNPTDLSBDLYLWVIPAARKNATVLIWYGGGFGT 120
 DB 89 YANSCQNAADSPFGHSEMMNPTDLSBDLYLWVIPAARKNATVLIWYGGGFGT 148
 QY 121 GTSSLYVDGKFLAVERIVYVSNRYGALGFALPBNPAPNGMGLFDQDLALQWQK 180
 DB 149 GTSSLYVDGKFLAVERIVYVSNRYGALGFALPBNPAPNGMGLFDQDLALQWQK 208
 QY 161 NIAAGGNPKSVTLRGESAGASVSLHLSPGSHSLFTRALIQSGSFNAPAVTSIYEAR 240
 DB 209 NIAAGGNPKSVTLRGESAGASVSLHLSPGSHSLFTRALIQSGSFNAPAVTSIYEAR 268
 QY 241 NRTLNIAKLTCGSRNTEIILKLNKDPQETILNEAFVVPYGPPLSVNFGPTVDGFLT 300
 DB 269 NRTLNIAKLTCGSRNTEIILKLNKDPQETILNEAFVVPYGPPLSVNFGPTVDGFLT 328
 QY 301 DMPDILLEIGOFKTKQILVGNKDKGTWFLVYGAGFGSDNNSITTRKPEOGKIFRPG 360
 DB 329 DMPDILLEIGOFKTKQILVGNKDKGTWFLVYGAGFGSDNNSITTRKPEOGKIFRPG 388
 QY 361 VSEFGKESILFYITWVDQRPENYREALGVGYNFICPALFETKXSEKGNNAFFY 420
 DB 389 VSEFGKESILFYITWVDQRPENYREALGVGYNFICPALFETKXSEKGNNAFFY 448
 QY 421 FEHRSKLPWPEMGVNGEIEFVGLPDERDNTYKAEILSSYKMANPKYGNP 480
 DB 449 FEHRSKLPWPEMGVNGEIEFVGLPDERDNTYKAEILSSYKMANPKYGNP 508
 QY 481 NETQNNSTSWPVKSTKQYTLNTESTRIMTKLRQOORFWTSFPPKYLWETGNIIDEAE 540
 DB 509 NETQNNSTSWPVKSTKQYTLNTESTRIMTKLRQOORFWTSFPPKYLWETGNIIDEAE 568
 QY 541 WEKAGFHRNNYMDKQNFNDYTSKESCVGL 574
 DB 569 WEKAGFHRNNYMDKQNFNDYTSKESCVGL 602

RESULT 6
 CHIE_PANTT STANDARD; PRT; 602 AA.
 AC 062761,
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudocholesterase)
 GN Name=CHIE;
 OS Panthera tigris tigris (Bengal tiger).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
 NCBI_Taxid=74535;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary; PubMed=10874122;
 RX MEDLINE=20334351; Pubmed=10874122;
 RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
 RA Lockridge O.;
 RT Determination of the DNA sequences of acetylcholinesterase and
 RT butyrylcholinesterase from cat and demonstration of the existence of
 RT both in cat plasma.
 RL Biochem. Pharmacol. 60:479-487(2000).
 CC -1- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -1- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
 CC two subunits in a dimer are linked by a disulfide bond (By
 CC similarity).
 CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
 CC organophosphate esters (By similarity).
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC
 CC EMBL: AF053484; AAC06262.1; -.
 DR HSSP: P22303; 1841.
 DR InterPro: IPR002018; CarboxylesteraseB.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser_estr.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR GlycoProtein: Hydrolase; Serine esterase; Signal.
 KW Glycoprotein; Hydrolase; Serine esterase; Signal.
 FT CHAIN 1
 FT ACT_SITE 29 602
 FT ACT_SITE 226 226
 FT ACT_SITE 353 353
 FT ACT_SITE 466 466
 FT DISULFID 93 120
 FT DISULFID 280 291
 FT DISULFID 428 547
 FT DISULFID 599 599
 FT CARBOHYD 85 85
 FT CARBOHYD 134 134
 FT CARBOHYD 269 269
 FT CARBOHYD 284 284
 FT CARBOHYD 369 369
 FT CARBOHYD 483 483
 FT CARBOHYD 509 509
 FT CARBOHYD 513 513
 FT CARBOHYD 514 514
 FT SEQUENCE 602 AA; 68289 MW; EB0CB9148B956A1 CRC64;

Query Match 86.3%; Score 2684; DB 1; Length 602;

Best Local Similarity 87.3%; Pred. No. 2.4e-193;
Matches 501; Conservative 23; Mismatches 50; Indels 0; Gaps 0;

QY 1 EDDIIITKNGKVGAMLVFGTGTATVAFGLPIYAOPPLGRLRFRKKPSLTKMSDINATK 60
D 29 EBDIIITTKNGKVGAMLVFGTGTATVAFGLPIYAOPPLGRLRFRKKPSLTKMSDINATK 88
QY 61 YANSCCONIDQSPFGFSGEMMNPNITLSEDCLYLWNIWAPKPKRNATVLIWYGGGFOR 120
D 89 HANSCYQNAQDSFGFGPSEMMNNTDSEDCLYLWNIWAPKPKRNATVLIWYGGGFOR 148
QY 121 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNMGLFDQALQWVOK 180
D 149 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNMGLFDQALQWVOK 208
QY 181 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFRALLOSGSFPAAPAVSLYEAR 240
D 209 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFRALLOSGSFPAAPAVSLYEAR 268
QY 241 NRTLNLAKLTGCSRENTEIICKLRNKPDEILNFAVVPYGTPLSVNFGPTVDGFLT 300
D 269 NRTLNLAKLTGCSRENTEIICKLRNKPDEILNFAVVPYGTPLSVNFGPTVDGFLT 328
QY 301 DMPDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKDNNSITTRKEFOGLKIFPPG 360
D 329 DMPDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKDNNSITTRKEFOGLKIFPPG 388
QY 361 VSEGEKSLIFHYDWDVDDORPENYREALGDVNDVNPICALFEYTKFSGWGNAPRY 420
D 389 VSEGEKSLIFHYDWDVDDORPENYREALGDVNDVNPICALFEYTKFSGWGNAPRY 448
QY 421 FEHSSKLPMPGEMVNGHYEIEFVGLPLERDNYTAEIISRSIVKRNAPKATGNP 480
D 449 FEHSSKLPMPGEMVNGHYEIEFVGLPLERDNYTAEIISRSIVKRNAPKATGNP 508
QY 481 NETONNSTWPFKSTOKYTLTTESTRTMTKLRPAQCFWTSFPKVLMTGNIDAE 540
D 509 NGTONNSTWPFKSTOKYTLTTESTRTMTKLRPAQCFWTSFPKVLMTGNIDAE 568
QY 541 WEMKAGFHRNNVMMMDKNOFNDYTSKESCVGL 574
D 569 WEMKAGFHRNNVMMMDKNOFNDYTSKESCVGL 602

RESULT 7
BAC34196 PRELIMINARY; PRT; 603 AA.
AC BAC34196;
DT 14-APR-2004 (TREMBlrel. 27, Created)
DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)
DE Adult male liver tumor cDNA, RIKEN full-length enriched library,
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hoti F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK050337; BAC34196.1; -; ZCB79C4679B3713 CRC64;
SQ SEQUENCE 603 AA; 68462 MW; 2CB79C4679B3713 CRC64;
Query Match 81.4%; Score 2530; DB 2; Length 603;
Best Local Similarity 80.7%; Pred. No. 9.6e-182;
Matches 463; Conservative 47; Mismatches 64; Indels 0; Gaps 0;
QY 1 EDDIIITKNGKVGAMLVFGTGTATVAFGLPIYAOPPLGRLRFRKKPSLTKMSDINATK 60
D 29 EBDIIITTKNGKVGAMLVFGTGTATVAFGLPIYAOPPLGRLRFRKKPSLTKMSDINATK 88
QY 61 YANSCCONIDQSPFGFSGEMMNPNITLSEDCLYLWNIWAPKPKRNATVLIWYGGGFOR 120
D 89 HANSCYQNAQDSFGFGPSEMMNNTDSEDCLYLWNIWAPKPKRNATVLIWYGGGFOR 148
QY 121 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNMGLFDQALQWVOK 180
D 149 GTSSLHYDGGKFLARVERVIVSMNRYGALGFLALPBNPAPGNMGLFDQALQWVOK 208
QY 181 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFRALLOSGSFPAAPAVSLYEAR 240
D 209 NIAAFGNPKSVTLFGSAGASVSLHLSGSHSLFRALLOSGSFPAAPAVSLYEAR 268
QY 241 NRTLNLAKLTGCSRENTEIICKLRNKPDEILNFAVVPYGTPLSVNFGPTVDGFLT 300
D 269 NRTLNLAKLTGCSRENTEIICKLRNKPDEILNFAVVPYGTPLSVNFGPTVDGFLT 328
QY 301 DMPDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKDNNSITTRKEFOGLKIFPPG 360

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Db 330 DMEHTLLQGLKVKKAQILVGVNDGEGTAFVVGAPSPSKDNDSLITRKEFGGLNNYFPG 389
Qy 361 VSEFGESLIEHTDWDDORPENYREALGDVVDNFCPALFEFTKSEWGNNAFFY 420
Db 390 VSLRGEAVLFYVDWLGESPEVYDADVDVGDNIICPALEFKKRAELENNAFFY 449
Qy 421 FEHRSSKLPWPEWNGVWGHGIEFVFGPLERRDNTYKAEILSRIVKMANFAYGNP 480
Db 450 FEHRSSKLPWPEWNGVWGHGIEFVFGPLERRDNTYKAEILSRIVKMANFAYGNP 509
Qy 481 NETONNSTSPVPEKSTOKLTNTSTRTMTLRAQOGRFWTSFPKYLEMNGINDAE 540
Db 510 NGTQNSTWMPVFTSTOKLTNTSTRTMTLRAQOGRFWTSFPKYLEMNGINDAE 569
Qy 541 WEMKAGFHRNNYMMQWQNFNDYTSKESCVGL 574
Db 570 QEMKAGFHRNNYMMQWQNFNDYTSKESCVGL 603

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RESULT 8

CHLE_MOUSE STANDARD; PRT; 603 AA.

```

AC 003311;
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholesterase).
GN Name=Behe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90380429; PubMed=2400605;
RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP SEQUENCE OF 97-237 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201148; PubMed=2016308;
RA Arpegans M., Chaconet A., Masson P., Newton M., Vaughan T.A.,
RA Barrels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: Homotrimer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond.
CC -1- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC -1- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M99497; AAA37328.1; -
CC FIP: S708497; S70849.
CC HSP: P22303; 1F8U.
CC MGI: MGI:894278; Behe.
CC InterPro: IPR002018; CarboxylesteraseB.

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DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser esters.
DR Pfam: PF00135; COESTERASE.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL
FT CHAIN 1 29
FT ACT_SITE 30 603
FT ACT_SITE 227 227
FT ACT_SITE 354 354
FT ACT_SITE 467 467
FT DISULFID 94 121
FT DISULFID 281 292
FT DISULFID 429 548
FT DISULFID 600 600
FT CARBOHYD 86 86
FT CARBOHYD 135 135
FT CARBOHYD 270 270
FT CARBOHYD 370 370
FT CARBOHYD 484 484
FT CARBOHYD 510 510
FT CARBOHYD 515 515
FT CONFLICT 129 129
SQ SEQUENCE 603 AA; 68521 MW; 719B1B2D0D1E367 C6C64;

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Query Match 81.1%; Score 2521; DB 1; Length 603;
 Best Local Similarity 80.5%; Pred. No. 4,6e-181;
 Matches 462; Conservative 47; Mismatches 65; Indels 0; Gaps 0;

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Qy 1 EDDIIATKNGKVRGMNLTVEGTTATFLGIPYAPRGLRPFKQSLTKMSDIWNTX 60
Db 30 EEDFIITTKTGVRGIGSMPEVLGIVTAFLGIPYAPRGLRPFKQSLTKMSDIWNTX 89
Qy 61 YANSCQNDIOSEPPGSGSEMNPNLSEDCLYANWIIPAKPKNAIVLWYGGGFOT 120
Db 90 YANSCQNDIOSEPPGSGSEMNPNLSEDCLYANWIIPAKPKNAIVLWYGGGFOT 149
Qy 121 GTSSLHVDKFLARVERIVYVSNRYGALGFLALPGNPEAPGNMGLPDQGLAQWQK 180
Db 150 GTSSLHVDKFLARVERIVYVSNRYGALGFLALPGNPEAPGNMGLPDQGLAQWQK 209
Qy 181 NIAPGNGPKSITLPEESAGASVSLHILSPGSHSLFTRALIQSGSPNAPNATSLYER 240
Db 210 NIAPGNGPKSITLPEESAGASVSLHILSPGSHSLFTRALIQSGSPNAPNATSLYER 269
Qy 241 NRTINLAKLTGCSRENTEIILKLRKQPOEILNBAFVVPYGTPLSVNFGFTVDGFLT 300
Db 270 NRTINLAKLTGCSRENTEIILKLRKQPOEILNBAFVVPYGTPLSVNFGFTVDGFLT 329
Qy 301 DMEHTLLQGLKVKKAQILVGVNDGEGTAFVVGAPSPSKDNDSLITRKEFGGLNNYFPG 360
Db 330 DMEHTLLQGLKVKKAQILVGVNDGEGTAFVVGAPSPSKDNDSLITRKEFGGLNNYFPG 389
Qy 361 VSEFGESLIEHTDWDDORPENYREALGDVVDNFCPALFEFTKSEWGNNAFFY 420
Db 390 VSLRGEAVLFYVDWLGESPEVYDADVDVGDNIICPALEFKKRAELENNAFFY 449
Qy 421 FEHRSSKLPWPEWNGVWGHGIEFVFGPLERRDNTYKAEILSRIVKMANFAYGNP 480
Db 450 FEHRSSKLPWPEWNGVWGHGIEFVFGPLERRDNTYKAEILSRIVKMANFAYGNP 509
Qy 481 NETONNSTSPVPEKSTOKLTNTSTRTMTLRAQOGRFWTSFPKYLEMNGINDAE 540
Db 510 NGTQNSTWMPVFTSTOKLTNTSTRTMTLRAQOGRFWTSFPKYLEMNGINDAE 569
Qy 541 WEMKAGFHRNNYMMQWQNFNDYTSKESCVGL 574
Db 570 QEMKAGFHRNNYMMQWQNFNDYTSKESCVGL 603

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RESULT 9

Q9JXCI

ID	PRELIMINARY;	PRT;	597 AA.
AC	09JUC1.		
AD	09JUC1.		
AE	01-OCT-2000 (TREMBLER). 15, Created)		
AF	01-OCT-2000 (TREMBLER). 15, Last sequence update)		
AG	01-OCT-2003 (TREMBLER). 25, Last annotation update)		
AH	Bucyricholnesterase.		
AI	Bucyricholnesterase.		
AJ	Bucyricholnesterase.		
AK	Bucyricholnesterase.		
AL	Bucyricholnesterase.		
AM	Bucyricholnesterase.		
AN	Bucyricholnesterase.		
AO	Bucyricholnesterase.		
AP	Bucyricholnesterase.		
AQ	Bucyricholnesterase.		
AR	Bucyricholnesterase.		
AS	Bucyricholnesterase.		
AT	Bucyricholnesterase.		
AV	Bucyricholnesterase.		
AW	Bucyricholnesterase.		
AX	Bucyricholnesterase.		
AY	Bucyricholnesterase.		
AZ	Bucyricholnesterase.		
BA	Bucyricholnesterase.		
BB	Bucyricholnesterase.		
BC	Bucyricholnesterase.		
BD	Bucyricholnesterase.		
BE	Bucyricholnesterase.		
BF	Bucyricholnesterase.		
BG	Bucyricholnesterase.		
BH	Bucyricholnesterase.		
BI	Bucyricholnesterase.		
BJ	Bucyricholnesterase.		
BK	Bucyricholnesterase.		
BL	Bucyricholnesterase.		
BM	Bucyricholnesterase.		
BN	Bucyricholnesterase.		
BO	Bucyricholnesterase.		
BP	Bucyricholnesterase.		
BQ	Bucyricholnesterase.		
BR	Bucyricholnesterase.		
BS	Bucyricholnesterase.		
BT	Bucyricholnesterase.		
BU	Bucyricholnesterase.		
BV	Bucyricholnesterase.		
BW	Bucyricholnesterase.		
BX	Bucyricholnesterase.		
BY	Bucyricholnesterase.		
BZ	Bucyricholnesterase.		
CA	Bucyricholnesterase.		
CB	Bucyricholnesterase.		
CC	Bucyricholnesterase.		
CD	Bucyricholnesterase.		
CE	Bucyricholnesterase.		
CF	Bucyricholnesterase.		
CG	Bucyricholnesterase.		
CH	Bucyricholnesterase.		
CI	Bucyricholnesterase.		
CJ	Bucyricholnesterase.		
CK	Bucyricholnesterase.		
CL	Bucyricholnesterase.		
CM	Bucyricholnesterase.		
CN	Bucyricholnesterase.		
CO	Bucyricholnesterase.		
CP	Bucyricholnesterase.		
CQ	Bucyricholnesterase.		
CR	Bucyricholnesterase.		
CS	Bucyricholnesterase.		
CT	Bucyricholnesterase.		
CU	Bucyricholnesterase.		
CV	Bucyricholnesterase.		
CW	Bucyricholnesterase.		
CX	Bucyricholnesterase.		
CY	Bucyricholnesterase.		
CZ	Bucyricholnesterase.		
DA	Bucyricholnesterase.		
DB	Bucyricholnesterase.		
DC	Bucyricholnesterase.		
DD	Bucyricholnesterase.		
DE	Bucyricholnesterase.		
DF	Bucyricholnesterase.		
DG	Bucyricholnesterase.		
DH	Bucyricholnesterase.		
DI	Bucyricholnesterase.		
DJ	Bucyricholnesterase.		
DK	Bucyricholnesterase.		
DL	Bucyricholnesterase.		
DM	Bucyricholnesterase.		
DN	Bucyricholnesterase.		
DO	Bucyricholnesterase.		
DP	Bucyricholnesterase.		
DQ	Bucyricholnesterase.		
DR	Bucyricholnesterase.		
DS	Bucyricholnesterase.		
DT	Bucyricholnesterase.		
DU	Bucyricholnesterase.		
DV	Bucyricholnesterase.		
DW	Bucyricholnesterase.		
DX	Bucyricholnesterase.		
DY	Bucyricholnesterase.		
DZ	Bucyricholnesterase.		
EA	Bucyricholnesterase.		
EB	Bucyricholnesterase.		
EC	Bucyricholnesterase.		
ED	Bucyricholnesterase.		
EE	Bucyricholnesterase.		
EF	Bucyricholnesterase.		
EG	Bucyricholnesterase.		
EH	Bucyricholnesterase.		
EI	Bucyricholnesterase.		
EJ	Bucyricholnesterase.		
EK	Bucyricholnesterase.		
EL	Bucyricholnesterase.		
EM	Bucyricholnesterase.		
EN	Bucyricholnesterase.		
EO	Bucyricholnesterase.		
EP	Bucyricholnesterase.		
EQ	Bucyricholnesterase.		
ER	Bucyricholnesterase.		
ES	Bucyricholnesterase.		
ET	Bucyricholnesterase.		
EU	Bucyricholnesterase.		
EV	Bucyricholnesterase.		
EW	Bucyricholnesterase.		
EX	Bucyricholnesterase.		
EY			

Db 504 NGTQGNSTVWVFVSTSEKTYLTLTATEKSKSKLRARQCCWRMRFPFVRLVETITODIDERE 563

QY 541 WEWKAQFHRNNVMMWYKQNFNDYTSKKESCVGL 574

Db 564 QEWKAGFFHRMSNYMMWKNQFNDYTSKKETCTDL 597

RESULT 10

Q90ZK8 PRELIMINARY; PRT; 603 AA.

ID Q90ZK8

AC Q90ZK8; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DR Butyrylcholinesterase precursor (EC 3.1.1.8).

GN Name=BCEH;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RM [1]

RP SEQUENCE FROM N.A.

RA Geisler K., Chatonnet A., Layer P.G.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -i- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

DR EMBL; AJ306928; CAC37792.1; -.

DR HSSP; P21836; INSM.

DR GO; GO:0004104; F:cholinesterase activity; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR InterPro; IPR002018; CarboxylesteraseB.

DR InterPro; IPR000997; Cholinesterase.

DR InterPro; IPR003179; Ser_estra.

DR Pfam; PF00135; Coesterase; 1.

DR PRINTS; PR00878; CHOLNSTRASE.

DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

DR Kwd Hydrolyase; Signal.

FT SIGNAL 1 29 Potential.

FT CHAIN 30 603 butyrylcholinesterase.

FT FT 603 603

SEQ SEQUENCE 603 AA; 68480 MW; A350DDDE8574ADF CRC64;

Query Match 73.6%; Score 2289; DB 2; Length 603;

Best Local Similarity 72.4%; Pred. No.1.4e-163;

Matches 414; Conservative 70; Indels 88; Gaps 0; Gaps 0;

QY 2 DDIIATNGKVRBMLTVPGCTATFLGIPYAPQPIGRIRFKKQSGSLTKMSDIWMATKY 61

Db 30 EDNVITTEKGVKRTNLQVLGGVTAFLGIPYGRPIGRIRFQKPEPEKWSGIWKATKH 89

QY 62 ANSCCONIDGSPFPFHGSEMMNPNTDISEDCLYANWAIIPAKPNATVLIWYGGGQTG 121

Db 90 ANSCQQLIDITTPGFPFGEMNPRTINISEDCLYANWAIIPSKPKNAIYMWIYGGSEFTG 149

QY 122 TSSLHYVDGKFLAVERIVVSNMYRVGALGFALPGNPPEAPGNMGLFDQGLALQWYQKN 181

Db 150 STSLPYVDGKFLAVERIVVSNMYRTGALGFALPGNKEVPGNAGLFDRLALQWYQEN 209

QY 182 IAAFGNPKSTLTLDGSENGASVSLHLSPSHSLFTRALIQSSFNAPAAVNSLYEARN 241

Db 210 IASFGNPKSTLTLDGSENGASVSYHLSPKSHPLFTRALMQSSANAPMALITASEARR 269

QY 242 RTLNLAKLTGCSRNENETIICKLNNKPOEFLINAEAVVPYGTPLSVNFGPTVDGDELTD 301

Db 270 RTVALAQAQKTPSDTEHLICLDKDPKDIENBEYVAVKFSLLHLYFCPTVDGDELAD 329

QY 302 MDLILLEGQPKKQIILVGNKDEGTMPLFYAGFGSKDNNSIITRKBPOBGLKIPPGV 361

Db 330 MPEALIKNGIKFQQLVAVGNKDEGTFILVYGVGFGSKDSLINTKQFEVALTLSPFPOV 389

QY 362 SEFGKESLFTYTQWVDQRPENVRRLAGVGVGNYNICPALBETTKFSEMGNAFFYYF 421

Db 390 SKAIESITFOYDMEWKEPEHYRDMVDVIGDHIICGAVFAKTLAEVGNVPEYFE 449

QY 422 EHRSSKLPMEWGVHGVYIEFVGLPLERDNYTKAEIILSRISVYKMANPAKGNPN 461

Db 450 EHRSSKLPMEWGVHGVYIEFVGLPLERDNYTKAEIILSRISVYKMANPAKGNPN 509

QY 482 ETONNSTSWVFSTOCKYTLTNTESRIMTKLRAOOCRWTSFPFVLEMTGNIDEAEW 541

Db 510 GTLLNGRMVFPSTOCKYTLTNTESRIMTKLRAOOCRWTSFPFVLEMTGNIDEAEW 569

QY 542 EMKAGFHRMNNYMDMKQFNDDYTSKKESCVG 573

Db 570 EMKAGFHRMNNYMDMKQFNDDYTSKKESCVG 601

RESULT 11

ACES BRARE STANDARD; PRT; 634 AA.

AC 09DDE3;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DB Acetylcholinesterase precursor (BC 3.1.1.7) (ACNE).

OS Name=ache;

GN Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20576389; PubMed=11016933; DOI=10.1074/jbc.M06308200;

RA Bertrand C., Chatonnet A., Takke C., Yan Y., Postlethwait J.,

RA Toulant J.-P., Cousin X.;

RT "Zebrafish acetylcholinesterase is encoded by a single gene localized on linkage group 7. gene structure and polymorphism; molecular forms and expression pattern during development";

RT J. Biol. Chem. 276:464-474(2001).

RL

CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.

CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.

CC -1- SUBUNIT: Dimers and collagen-tailed forms, in which catalytic tetramers are associated with anchoring proteins that attach them to the basal lamina or to cell membranes. In the collagen-tailed forms, subunits are associated with a specific collagen, COLQ, which triggers the formation of isoform T tetramers from dimers.

CC -1- MISCELLANEOUS: No other isoforms exist. This protein corresponds to the T isoform in other species.

CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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CC -----

CC EMBL; AJ251640; CAC19790.1; -.

DR HSSP; P04058; 1H23.

DR ZFIN; ZDB-GENE-010906-1; ache.

DR InterPro; IPR002018; CarboxylesteraseB.

DR InterPro; IPR000997; Cholinesterase.

DR InterPro; IPR000379; Ser esters.

DR Pfam; PF00135; Coesterase; 1.

DR PRINTS; PR00878; CHOLINESTRASE.

DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

DR Glycoprotein; Hydroxylase; Membrane; Neurotransmitter degradation;

KW Serine esterase; Signal; Synapse.

FT SIGNAL 1 23 Potential.

FT CHAIN 24 634 Acetylcholinesterase.

FT ACT_SITE 225 225 Acyl-ester intermediate (By similarity).

FT ACT_SITE 352 352 Charge relay system (By similarity).

FT ACT SITE 495 495 Charge relay system (By similarity).

FT DISULFID 91 118 By similarity.

FT DISULFID 279 290 By similarity.

FT DISULFID 427 580 By similarity.

FT DISULFID 631 631 Interchain (By similarity).

FT CARBOHYD 133 133 N-linked (GlcNAc...) (potential).

FT CARBOHYD 184 184 N-linked (GlcNAc...) (potential).

FT CARBOHYD 283 283 N-linked (GlcNAc...) (potential).

FT CARBOHYD 368 368 N-linked (GlcNAc...) (potential).

FT CARBOHYD 512 512 N-linked (GlcNAc...) (potential).

FT CARBOHYD 592 592 N-linked (GlcNAc...) (potential).

SQ SEQUENCE 634 AA; 71998 MW; 47F348BA87C1E52 CRC64;

Query Match 56.8%; Score 1765.5; DB 1; Length 634;

Best local similarity 53.0%; Pred. No. 3.9e-124;

Matches 323; Conservative 106; Mismatches 144; Indels 37; Gaps 6;

QY 1 EDDIIATKNGKVRGMNLTVFGGT-VTAFGLFYPYQPLGRAPKKPQSLTWSIDIMNT 59

Db 26 EPDLVATRLAGVOGTRLPVDPDRSHVIAFLGIPYAEPPGKRRFAEPKKEMNWPEAK 85

QY 60 KYANSCCONIDOSPFGHSEEMNPNTDSEDCLYLNTWVI-DAPPKNATVLIWYGGGF 118

Db 86 ERSNACTQYVDTSYGPFPGIEMNPNRWSEDCLYLNTWVPPTPRQNLTVWVWYIGGSF 145

QY 119 QTGTSILHYDGEKFLARVERVIVSMNYVGAAGLALPGNPEAPQNMGLFPQQLALQWY 178

Db 146 YSGSSSLDYVDGRYLAYTEKVVVSMNYVGAAGLALPGNPEAPQNMGLFPQQLALQWY 205

QY 179 QKNIAAFGNGPKSVTLFGSSAGAAVSLLSLSPGSHLFTRAILLGSGFNAPNATVSLY 238

Db 206 QENIHFFGNGPKSVTLFGSSAGAAVSLLSLSPGSHLFTRAILLGSGFNAPNATVSLY 265

QY 239 ARNRRTNLAKLTCGSRNETETIICLRNKPQELILNEAFVVPYGTPLSVNFGPTVDGF 298

Db 266 ARNRRTNLAKLTCGSRNETETIICLRNKPQELILNEAFVVPYGTPLSVNFGPTVDGF 325

QY 299 LITMDPILLETGQFKTQILVGNKDEGTWFLVYGAPGFSKONNSITTKPEQEGIKTF 358

Db 326 FPDTPPAMTSSGFKTQILVGNKDEGTWFLVYGAPGFSKONNSITTKPEQEGIKTF 385

QY 359 PGVSEFGKESILFHYTDWDQDPENYREALGVGDVNYPCALFEFTKFSF----- 411

Db 386 PHANDIGLEAVLIQYTDMDENNQGNRDMDDVDQVNICLQHPAASYAOYALAHQ 445

QY 412 -----WGNN-----AFYYFEHRSSKLPMEWGVHGVYIEFVGL 448

Db 446 SSAARPTLGMGSGPTGVNNGSHGAVYILFDHRAASNLAMPEWGVHGVYIEFVGL 505

QY 449 PLERDNYTKAEIILSRISVYKMANPAKGNPN-----ETONNSTSWVFSTOCKYTLTN 504

Db 506 PLERDNYTKAEIILSRISVYKMANPAKGNPN-----ETONNSTSWVFSTOCKYTLTN 565

QY 505 TESTRIMTKLRAOOCRWTSFPFVLEMTGNIDEAEWEMVHRMNNYMDMKQFNDDY 564

Db 566 TESTRIMTKLRAOOCRWTSFPFVLEMTGNIDEAEWEMVHRMNNYMDMKQFNDDY 625

QY 565 TSKKESCVGL 574

Db 626 -SKQERCTDL 634

RESULT 12

ACES EMBL STANDARD; PRT; 633 AA.

AC 042275;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DB Acetylcholinesterase precursor (BC 3.1.1.7) (ACNE).

OS Electrophorus electricus (Electric eel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;

CC Electrophoridae; Electrophorus.
 OX NCBI_Taxid=8005;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98070504; PubMed=9407087;
 RA Simon S., Massoulie J.
 RT "Cloning and expression of acetylcholinesterase from Electrophorus.
 RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
 RT cells.";
 RL J. Biol. Chem. 272:33045-33055 (1997).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF030422; AAB86606.1; -
 DR HSPB: P04058; I123.
 DR InterPro: IPR002018; CarbesteraseB.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser estse.
 DR Pfam: PF00135; Coesterase: 1.
 DR PRINTS: PR00878; CHOLINESTRASE.
 DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
 KM Glycoprotein; Hydrolyase; Membrane; Neurotransmitter degradation;
 KM Serine esterase; Signal; Synapse.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 633 Acetylcholinesterase.
 FT ACT_SITE 225 325 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 352 352 Charge relay system (By similarity).
 FT ACT_SITE 494 494 Charge relay system (By similarity).
 FT DISULFID 91 118 By similarity.
 FT DISULFID 279 290 By similarity.
 FT DISULFID 427 579 By similarity.
 FT DISULFID 630 630 Interchain (By similarity).
 FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;
 Query Match 56.8%; Score 1765; DB 1; Length 633;
 Best Local Similarity 53.2%; Pred. No. 4.3e-124;
 Matches 324; Conservative 103; Mismatches 146; Indels 36; Gaps 6;
 QY 1 EDIIITATKQKGVKGMNLYFGGT-VTAFLGIPYAOPPLGLRKPKQSLTKMSDINWAT 59
 DB 26 DPELTITMRLGQVGQTRLPVDRSHVLAFLGIPFAEPPLGMRKPKPEKPMWDVDFAR 85
 QY 60 KYANSCQNDIQSPFGHSGEMNPNTDLSBDCIYLVNMPA-RPKKATYLVITYGGEF 118
 DB 86 DYPACQYQYDTSYPGFSGTEMMNPNRMWSEDCIYLVNMPATRPFHLTYVMVITYGGEF 145
 QY 119 QYTGSSLVHVDGKRLAVERTIVSMYRVAGLFLALPGRPBAPGMNGLPDQDLALQWV 178
 DB 146 YSGSSSLDVVDGKRLAVERTIVSMYRVAGLFLALPGRPBAPGMNGLPDQDLALQWV 205
 QY 179 QKNIATAGNPKSYTLTGESAGAAVSILHLSFSGSHLFTRAIIQSGSFNAPMAVTSIYE 238
 DB 206 QDNTHFGGNPKQYTLTGESAGAAVSILHLSFSGSHLFTRAIIQSGSFNAPMAVTSIYE 265
 QY 239 ARNATLAKLTGSGRENETIILKLRNKPQQLLNEAFVVPYGTPLSVNFGTVDGDF 298
 DB 266 ARRAIKLGRIVGCPDNDTDLIDCLRSKOPDIDQEMVLPSGGLFRFSFVVIDGVV 325

QY 299 LTDMPIILLEGQFKTQIIVGVNKGDTWFLVYAGFSGKDNNSITTRKEFGGLKIF 358
 DB 326 FPDTPPEAMLSGNFKDQIILGVNKGESYFLIYGAFSGKDNNSITTRKEFGGLKIF 385
 QY 359 PGUSEFKESELPHYTDWVDORPENREALGVDGVYNYICPLAETTKFSF----- 411
 DB 386 PHANEIGLEAVIILQYTDWMDENPDKRREAMDIVGHNVCPLQHFARKYAOYSIIQOQ 445
 QY 412 -----MGN-----NAFYFPHRSKLPMPWGMVGHGIEFVGLP 449
 DB 446 TGRASQNLGWSGASNSGNSQSVSYLYMFDHRASNLVWPEMGVIHGEIEFVGLP 505
 QY 450 LERRDNTYKAEILSRISIVKMANFAYKGNPNETONNSTS-----WPVFKSTQKYLTLNT 505
 DB 506 LERKINLTLEBEKLSRMKMYMANFATGNPINVDGSISSRRWPVFTSTQGHVGLNT 565
 QY 506 ESTRIKTKRAQOCRFPTSFPPKYLENTGIDAEWVKAGFHRMNNYMDKQFNDYT 565
 DB 566 DSLKVRHGLKSFQCALWNRPLPRLVNTENIDDAERQWKAEPFRWSSYMMWKNQFDHY- 624
 QY 566 SKKSCVGL 574
 DB 625 SKQERCTNL 633
 RESULT 13
 ACES_BUNFA STANDARD; PRT; 606 AA.
 ID ACES_BUNFA STANDARD; PRT; 606 AA.
 AC Q92035; Q73748; Q10720;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Acetylcholinesterase precursor (BC 3.1.1.7) (AChE).
 OS Bungarus fasciatus (Banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungariinae; Bungarus.
 OX NCBI_Taxid=6613;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM S).
 RC TISSUE=Venom gland;
 RX MEDLINE=96279007; PubMed=8662867;
 RA Cousin X., Bon S., Massoulie J., Bon C.;
 RT "Cloning and expression of acetylcholinesterase from Bungarus
 RT fasciatus venom. A new type of COOH-terminal domain; involvement of a
 RT positively charged residue in the peripheral site.";
 RL J. Biol. Chem. 271:15099-15108 (1996).
 RN [2]
 RP SEQUENCE OF 512-606 FROM N.A. (ISOFORMS S AND T), SUBUNIT, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Liver, and Muscle;
 RX MEDLINE=98212017; PubMed=9545320;
 RA Cousin X., Bon S., Massoulie J., Bon C.;
 RT "Identification of a novel type of alternatively spliced exon from the
 RT acetylcholinesterase gene of Bungarus fasciatus. Molecular forms of
 RT acetylcholinesterase in the snake liver and muscle.";
 RL J. Biol. Chem. 273:9812-9820 (1998).
 RN [3]
 RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.
 RC TISSUE=Venom;
 RX MEDLINE=96244524; PubMed=8674549;
 RA Cousin X., Cremonon C., Grassi J., Meflah K., Cornu G., Sallou B.,
 RA Bon S., Massoulie J., Bon C.;
 RT "Acetylcholinesterase from Bungarus venom: a monomeric species.";
 RL FEBS Lett. 387:196-200 (1996).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,
 CC including collagen-tailed forms.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Name=T;
CC IsoId=Q92035-2; Sequence=Displayed;
CC Name=S;
CC IsoId=Q92035-1; Sequence=VSP 008215;
CC TISSUE SPECIFICITY: Liver and muscle contain both isoform T and
CC isoform S. Venom gland predominantly contains isoform S.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
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DR EMBL, U54591, AAC59905.1, -.
DR EMBL, AF045238, AAC16420.1, -.
DR EMBL, AF045238, AAC16421.1, -.
DR HSSP, P04058, 1H23.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000908; Fish_Ache.
DR InterPro: IPR000379; Ser_estre.
DR Pfam, PF00135, Coesterase, 1.
DR PRINTS, PR00878, CHOLNESTRASE.
DR PROSITE, PS00122; CARBOXYLESTERASE B_1; 1.
DR PROSITE, PS00941; CARBOXYLESTERASE B_2; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydroxylase; Membrane; Neurotransmitter degradation; Serine esterase;
KW Signal; Synapse.

FT SIGNAL 1
FT CHAIN 1
FT ACT_SITE 29
FT ACT_SITE 231
FT ACT_SITE 358
FT ACT_SITE 471
FT DISULFID 98
FT DISULFID 285
FT DISULFID 433
FT DISULFID 603
FT CARBOHYD 289
FT CARBOHYD 374
FT CARBOHYD 484
FT CARBOHYD 564
FT VARSPLIC 567
FT MUTAGEN 101
FT MUTAGEN 316
FT CONFLICT 268
FT CONFLICT 350
FT SEQUENCE 606 AA; 68074 MW; B95999AEEA05E709 CRC64;

Query Match 55.4%; Score 1722.5; DB 1; Length 606;
Best Local Similarity 52.9%; Pred. No. 6.4e-121;
Matches 301; Conservative 110; Mismatches 157; Indels 1; Gaps 1;

3 DIIITKNGKXKRGMLTVRGGVTAFLGIPYAPLGLRPFKKPSLTKMSIMNATCYA 62
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
36 ELKAVTQTSVAGSLPLVDGHSAPLGLIPFAEPFLGKRFLRPPVPVPMQVHDATSYK 95
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
63 NSCCNIDQSPGFGSEMMNNTDLSEDCLYLNVWIPAPKPKNAITVIMYGGGFGTGT 122
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
96 PACYQWVDTSYSGFGQTEKMNENRGMSEDCLYLTIWVSPRDKAPVLIWYIGGGFYSGA 155
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
123 SGLHYTDGFLARVERIVYVSNRYVAGLALGNGNPAPNMGILFOQALQWVQNI 182
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
156 ASLDVYDGRFLTYTONVILVSLSYRVGAGFLGLPSGPPAPNMGILDQRLALQNI 215
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

QY 183 AAFGNPKSVTLFGESAGASVSLHLSPGSHLFTRAILQSGSNAPAVTSIYEARNR 242
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 216 HFFGNPRAVTVFGESAGASVGMHLSTQSRITLFRAILQSGGNAPAVTAPESNGR 275
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 243 TLNLAKLTGCSRENETETIKLRNKPQELILNEAFVVPYGTPLSVNFGPLVDGFLTDM 302
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 276 AALLKQJGCHNRNDSVLSGRSKNPQELIDEMSVLPYKSIFFPPVPVLDGDFPFD 335
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 303 PILLLELQPKTKTQLLVGNVNDGEGTWPLVYGAPGSKNNISITPKKEQEGIKTFFPVS 362
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 336 PAMLSVGNFKETQVLLGVNDGSGYFLILYGLPGSKNESLISADLVGRNVPAN 395
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 363 EFGKESILFHYTDWDDQRPENYREALGVVDVYFICPALFTFKFSFGNNAFFYYE 422
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 396 DIATDAVVIQYTDMDQDNREKRALDDIYGDHVICPVQFANDYAKRNSKVAYLFD 455
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 423 HRSKLPWEMWGVNMGYIEFVFGPLERRDNYTKABEILSRSLVKMANPAKGNPNE 482
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 456 HRASNLMPFMVGVPHGEIEFVFGPLINDSLNTPQEKELSRMMRYMANPARGNPTD 515
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 483 TQNNSTSWVFKESTOKTILNTTESTRLMTKLRAQCFPMTSFPFKVLEMTGNIDEAWE 542
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 516 PDKSGAMPTVYASQPVQVLTQPLATQPSLRAGI CAFWNHFPLRLNATNIDEARQ 575
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
QY 543 WKAGFRRNNVMMWKNQFNDYTSKKESC 571
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 576 WLEFFILMSAYMMHMSQPDHY-NKQDRC 603
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 14
ACES_HUMAN
ID ACES_HUMAN STANDARD; PRT; 614 AA.
AC P22303; Q16169; Q9BXPT;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
ON NCBI_TaxId=9606;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2118439; PubMed=2263619;
RA Soreg H., Ben-Aziz R., Prody C.A., Seidman S., Gnat A., Neville L.,
RA Lleman-Hurwitz J., Lev-Lehman E., Ginsberg D., Lipidot-Litson Y.,
RA Zakut H.;
RT "Molecular cloning and construction of the coding region for human
RT acetylcholinesterase reveals a G + C-rich attenuating structure.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RL [2]
RN SEQUENCE OF 521-614 FROM N.A.
RP MEDLINE=2118439; PubMed=11239002;
RX Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Borright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsai L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHR/TFP2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RT Nucleic Acids Res. 29:1352-1365(2001).
RL [3]
RN PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RP MEDLINE=94131004; PubMed=8299725;
RX Karpel R., Ben Aziz-Aluya R., Sternfeld M., Ehrlich G., Ginsberg D.,
RA Taroni P., Clementi F., Zakut H., Soreg H.;
RT "Expression of three alternative acetylcholinesterase messenger RNAs
RT in human tumor cell lines of different tissue origins.";
RT Exp. Cell Res. 210:268-277(1994).
RL [4]
RN PARTIAL SEQUENCE.
RP TISSUE=Erythrocyte;
RX MEDLINE=89232136; PubMed=2714437;

ID	ACCS	RAT	STANDARD;	PRT;	614	AA.
AC	P37136;					
DT	01-OCT-1994	(Rel. 30, Created)				
DT	01-OCT-1994	(Rel. 30, Last sequence update)				
DT	01-OCT-2004	(Rel. 45, Last annotation update)				
DE	Acetylcholinesterase	precursor (EC 3.1.1.7) (ACHE).				
GN	Name=Ache;					
OS	Rattus norvegicus (Rat).					
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORM T).					
RA	MEDLINE=93107932; PubMed=8417155;					
RT	Legacy C., Bon S., Vernier P., Cousen F., Massoulié J.;					
RT	"Cloning and expression of a rat acetylcholinesterase subunit:					
RT	generation of multiple molecular forms and complementarity with a					
RT	Torpedo collagenic subunit."					
RL	J. Neurochem. 60:337-346(1993).					
RN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORMS H AND R).					
RA	MEDLINE=93114454; PubMed=8417973;					
RT	Legacy C., Bon S., Massoulié J.;					
RT	"Expression of a cDNA encoding the glycolipid-anchored form of rat					
RT	acetylcholinesterase."					
RL	FEBS Lett. 315:163-166(1993).					
CC	-1- FUNCTION: Rapidly hydrolyses choline released into the synapse.					
CC	-1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.					
CC	-1- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.					
CC	Catalytic forms H (GPI-anchor dimer) and T (asymmetric collagen-					
CC	tailed), which differ in their C-terminus, account for all types					
CC	of known AChE forms. Interacts with PRIMA1. The interaction with					
CC	PRIMA1 is required to anchor it to the basal lamina of cells and					
CC	organize into tetramers (By similarity).					
CC	-1- ALTERNATIVE PRODUCTS:					
CC	Event=Alternative splicing; Named isoforms=3;					
CC	Name=T;					
CC	IsoId=P37136-1; Sequence=Displayed;					
CC	Name=H;					
CC	IsoId=P37136-2; Sequence=VSP_001458;					
CC	Name=R;					
CC	IsoId=P37136-3; Sequence=VSP_001455;					
CC	Note=May be not functional;					
CC	-1- TISSUE SPECIFICITY: Has been found in central nervous system and					
CC	muscle. Found in embryonic liver and spleen but not in adult					
CC	liver.					
CC	-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.					
CC	-----					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce					
CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; S50879; AAB24586.1; -;					
DR	EMBL; X70140; CAA49717.1; -;					
DR	EMBL; X70141; CAA49718.1; -;					
DR	PIR; JH0811; JH0811.					
DR	HSSP; P21836; IMAA.					
DR	RGD; 69313; Ache.					
DR	InterPro; IPR002018; Carboxylesterase.					
DR	InterPro; IPR000997; Cholinesterase.					
DR	InterPro; IPR000379; Ser_eastsr.					
DR	Pfam; PF00135; Coesterase; 1.					
DR	PRINTS; PR00878; CHOLINESTRASE.					
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.					
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.					
KW	Alternative splicing; Glycoprotein; Hydrolase; Membrane;					
KW	Neurotransmitter degradation; Serine esterase; Signal; Synapse.					
FT	SIGNAL	1	31			Potential.
FT	CHAIN	32	614			Acetylcholinesterase.

FT	ACT_SITE	234	234	ACT-ester intermediate (By similarity).
FT	ACT_SITE	365	365	Charge relay system (By similarity).
FT	ACT_SITE	478	478	Charge relay system (By similarity).
FT	DISULFID	100	127	By similarity.
FT	DISULFID	288	303	By similarity.
FT	DISULFID	440	560	By similarity.
FT	DISULFID	611	611	Interchain (By similarity).
FT	CARBOHYD	296	296	N-linked (GlcNAc. . .) (potential).
FT	CARBOHYD	381	381	N-linked (GlcNAc. . .) (potential).
FT	CARBOHYD	495	495	N-linked (GlcNAc. . .) (potential).
FT	VARSPLIC	575	614	DTLDAERQMKAEFFHRMSYSYVMHKNQDFHYSKQERCSDL -> ATEVECTCPSPAHGEAAPPAPALSLSLFLLHSG LRWL (in isoform H).
FT				/FTID=VSP 001458.
FT	VARSPLIC	575	614	DTLDAERQMKAEFFHRMSYSYVMHKNQDFHYSKQERCSDL -> GRRGVKQOMHKAARVGRTERGKGGKHM (in isoform M).
FT				/FTID=VSP 001459.
SEQ	SEQUENCE	614 AA;	68196 MM;	2EDAE7D46282E7C0 CRC64;
Query Match		54.0%;	Score 1678.5;	DB 1; Length 614;
Best Local Similarity		53.1%;	Pred. No. 1.3e-117;	
Matches 308;	Conservative	102;	Mismatches 163;	Indels 7; Gaps 4
QY	1	EDDIIIAKNGKVRGMNLTVGCGTAAFLGIFPAQPRGLRAFFKKRQSLTKKSDIMNARK	60	
DB	36	DPQILLVRRGQGLRIRIKRAPGSPASLGIIPFAEPVPSRRFMPPEPRPSSGIIIDATT	95	
QY	61	YANSCCVINDSPFGHSEMMNPNTDISEDCLYTNWVIPARKPKNAAT-VLIWYGGGQ	119	
DB	96	FQNVCTYQVVDLILYFPEEGTEMMNPREISEDCLYTNWTPYRPRPSPTVLWLYGGGQ	155	
QY	120	TGTSLSHYADKFLARVERVIVSNMYRVGALGFLALPGNPPAEGMGLFDQALQWQ	179	
DB	156	SGASLDVYDGRFLAQVEGTVLVSNMYRVGTGFALPGSRAPAGVGLDQRLAQWQ	215	
QY	180	KNIAAFGNGPKSVTLFGESAGAASVSLHLSGSGHSLPRALLOGSGFPAAPAVNLSYEA	239	
DB	216	ENIAAFGADPMSVTLFGESAGAASVGMHLSLPSRLFAVALQSGTPNGPAVYASGA	275	
QY	240	RNRTLNLAKLQGC---GRENTEITIKCLRNDDPOEILLNEAFVYPGTPPLSNFGPTVD	295	
DB	276	RRRATILRLVLCGPPGAGAGNDTEISCLRTPRADDLVDHEHNLVPOESIPRPSFPVVD	335	
QY	296	GDFLTMDIDILLEGQFKKTQILVGNVNDGDTFLVYAGFSGKNNSSIIITREFOEGLK	355	
DB	336	GDFLSDTQDALINTGDFDQLVGLVGVNDGEGSYFLVYGVGRSKNNESLISRAQFLAVR	395	
QY	366	IFPFEVSGFPGKSLIFHTTDMVDQDPRPNRYALADGVYGVYIFCPALEFTKKFSWGN	415	
DB	396	IGVPQASDILAAVAVLHYATYDMVLPHPDPAHLRPAMAAVVDHNVCPVALAGRLAAQGR	455	
QY	416	AFPYFEEHRSKGLPPEMVGWNGHGEIEFVGLPLPERRDNYTKAEELISRYIKRANPA	475	
DB	456	VYATYFEEHRSALTLMPPLMWGVPHGHEIFITFELPLDPSLANTYVEERITPQRLAQYTNA	515	
QY	476	KYGNENETQNN-STSWPVFKSTEQKYLTLNTESTRIMTKLAAQOCRFWTSFFPKVLEMTG	534	
DB	516	RTGDNDNRDSDKSPRPWPYTTAAQOQYSLNKLPLEVRGLRQOTCAFMRFLPKLSATD	575	
QY	535	NIDEAEWEMKAGFHRMNNYMDMKQNFNDYTSKESCVGL	574	
DB	576	TLDEAEQMKAEFFHRMSYSYVMHKNQDFHY-SKQERCSDL	614	
RESULT 17				
ID	ACES_MOUSE	STANDARD;	PRT;	614 AA.
AC	P21836;			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Acetylcholinesterase precursor (E.C.3.1.1.7) (Ache).			

GN Name-Ache;
 OS Mus musculus (house).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90380429; PubMed=2400605;
 RX Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species.";
 RL Neuron 5:317-327(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=2118439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boitight A.P.,
 RA Cheung T.L., Hardy D.W., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.P.;
 RT "Comparative analysis of the gene-dense AChE/TFP2 region on human
 chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge U.G.,
 RA Strauss R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Canninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting R., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP INTERACTION WITH PRIMA1.
 RX MEDLINE=21664287; PubMed=11804574;
 RA Perrier A.L., Massoulié J., Krejci E.;
 RT "PRIMA1, the membrane anchor of acetylcholinesterase in the brain.";
 RL Neuron 33:275-285(2002).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE=96067648; PubMed=8521480;
 RA Bourne Y., Taylor P., Marchot P.;
 RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
 the complex.";
 RL Cell 83:503-512(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99115643; PubMed=9915834;
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
 including loop in a tetrameric assembly.";
 RL J. Biol. Chem. 274:2963-2970(1999).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 34-573 IN COMPLEX WITH
 RP INHIBITOR.
 RX Pubmed=12505979; DOI=10.1093/emboj/cdg005;
 RA Bourne Y., Taylor P., Radic Z., Marchot P.;
 RT "Structural insights into ligand interactions at the
 acetylcholinesterase peripheral anionic site.";

RL EMBO J. 22:1-12(2003).
 CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: Isoform H generates GPI-anchored dimers; disulfide
 CC linked. Isoform T generates multiple structures, ranging from
 CC monomers and dimers to collagen-tailed and hydrophobic-tailed
 CC forms, in which catalytic tetramers are associated with anchoring
 CC proteins that attach them to the basal lamina or to cell
 CC membranes. In the collagen-tailed forms, isoform T subunits are
 CC associated with a specific collagen, COLQ, which triggers the
 CC formation of isoform T tetramers, from monomers and dimers (by
 CC similarity). Interacts with PRIMA1. The interaction with PRIMA1 is
 CC required to anchor it to the basal lamina of cells and organize
 CC into tetramers.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=T;
 CC IsoId=P21836-1; Sequence=Displayed;
 CC Name=H;
 CC IsoId=P21836-2; Sequence=Not described.
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Predominates in most expressing tissues except
 CC erythrocytes where a glycopospholipid-attached form of AChE
 CC predominates.
 CC -1- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
 CC cholinesterase, with a collagen-like part disulfide-bonded to the
 CC catalytic part. A different, globular type of cholinesterase
 CC occurs on the outer surfaces of cell membranes, including those of
 CC erythrocytes. This is the catalytic subunit of an asymmetric or
 CC soluble form of AChE.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X65518; CA39867.1; --
 CC EMBL: AF312033; AA02816.1; --
 CC EMBL: BC046327; AA046327.1; --
 CC PIR: JH0314; JH0314.
 CC PDB: 1C2B; X-ray; A=35-573.
 CC PDB: 1C2O; X-ray; A/B/C/D=36-574.
 CC PDB: 1U06; X-ray; A/B=32-574.
 CC PDB: 1U07; X-ray; A/B=32-574.
 CC PDB: 1XU6; X-ray; A=32-580.
 CC PDB: 1MAA; X-ray; A/B/C/D=32-578.
 CC PDB: 1MAH; X-ray; A=32-574.
 CC PDB: 1NSW; X-ray; A/B=32-572.
 CC PDB: 1NSR; X-ray; A/B=32-574.
 CC PDB: 1Q83; X-ray; A/B=1-580.
 CC MGD: MGI:87876; Ache.
 CC GO: GO:0045202; C:synapse; IDA.
 CC InterPro: IPR002018; Carboxylesterase.
 CC InterPro: IPR000997; Cholinesterase.
 CC InterPro: IPR000379; Ser_estrs.
 CC Pfam: PF00135; Coesterase_1.
 CC PRINTS: PR00878; CHOLINESTRASE.
 CC PROSITE: PS00122; CARBOXYLESTERASE B 1, 1.
 CC PROSITE: PS00941; CARBOXYLESTERASE B 2, 1.
 CC 3D-structure: Alternative splicing; Glycoprotein; Hydrolase; Membrane;
 CC Neurotransmitter degradation; Serine esterase; Signal; Synapse.
 CC SIGNAL
 CC CHAIN 32 614 Acetylcholinesterase.
 CC ACT_SITE 234 234 Acyl-ester intermediate.
 CC ACT_SITE 365 365 Charge relay system.
 CC ACT_SITE 478 478 Charge relay system.
 CC DISULFID 100 127
 CC DISULFID 288 303

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FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT HELIX 37 39
FT STRAND 40 43
FT TURN 44 45
FT STRAND 46 49
FT STRAND 51 55
FT TURN 56 57
FT STRAND 58 67
FT STRAND 69 69
FT HELIX 74 76
FT TURN 77 78
FT STRAND 83 83
FT STRAND 90 92
FT STRAND 94 94
FT STRAND 99 100
FT TURN 109 110
FT HELIX 112 115
FT TURN 116 117
FT STRAND 123 124
FT STRAND 129 135
FT STRAND 143 149
FT TURN 153 155
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FT TURN 245 245
FT HELIX 247 250
FT STRAND 251 252
FT STRAND 255 259
FT STRAND 270 271
FT HELIX 272 285
FT TURN 286 287
FT HELIX 297 304
FT TURN 305 306
FT HELIX 309 315

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Interchain (By similarity).
N-linked (GlcNAc...) (Potential).
N-linked (GlcNAc...).
N-linked (GlcNAc...).

Query Match 53.9%; Score 1675.5; DB 1; Length 614;
Best Local Similarity 52.8%; Pred. No. 2,3e-117;
Matches 306; Conservative 104; Mismatches 163; Indels 7; Gaps 4;

```

QY 1 EDDIIATKNGKVGKMLTVFGGTVAFLGIPYAPPLGRLRFKKPSLTKMSDIMNATK 60
DB 36 DPOLIVVRGQRLRGIRLKAAPGVSAPLGPAPPPGSRFPMPPEPKPMSGVLDATT 95
QY 61 YANSCCNINQSPFGHSEMMNNTLSBCLYLNWIPAKPKKAT-VLIWYGGGFQ 119
DB 96 FQNVQYVDTLPGFEGTEMMNRELSEDCYLNWTPPRPASLPTVLIWYGGGFY 155
QY 120 TGTSLHYDGKFLARVIVSMNRYGALGFALPGNPEAPGNKGLFDOQLALQWVQ 179
DB 156 SGAAASLDVYGRFLAIVEGAVIVSMNRYGTFGLALPGSREAPGNVGLDORLALQWVQ 215
QY 180 KNIAAFGNGKSVTLTFESAGASVSLHLSPGSHSLPTPAITLQSGSFNAPWAVTSLEYA 239
DB 216 ENIIAAGFQDMSVTLTFESAGASVGMHILSLPERSLFHRAVLQSGTPNGPMATVSAGEA 275
QY 240 RNTTILNKLITGC---SRNETETIKCLRNKDPQELLNEAFVVPYGTPLSVNGFPTVD 295
DB 276 RRRATLRLVGGPPGAGGNDYELLACLRTPRADLVDEHMYLPOESIFRFSEFVVD 335

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QY 296 GDFITMDPILILEGCKKQIILYGVNKKDGTWFLVYGAQFGSKDNNSITTRKEFORGLK 355
DB 336 GDFSLDPPEALINTGDDQDQVLVGVVKKDGSYFLVGVGFSKDNLSLSRAQFLAGVR 395
QY 356 IFFPGVSEPKESILFHYTQWVDQRENTREBALGVDVGVNFCPLLEFTKKSEMGNN 415
DB 396 IGVFOASDILAEAVLHYTTLHPEDPTLURDMSAVGVNDHNVCPAQLAGRLAAGAR 455
QY 416 AFYFFFEHRSKSLPWPMMGMVHGYEIEFVFGHPLERNDVYTKAEILSRIVRWANFA 475
DB 456 VYAIIFHRASLTLPVPMGVPHCYEIEFIFGLPLDSLYNTTBERTFAQRLMKYWNFA 515
QY 476 KYGNPNETQNN-STSWPVEKSTQKYTLTNTSTRTMTKLRQAQCRFTSPFPKVLMTG 534
DB 516 RTGDPNDPDSKSPQWPPYTTAAQVYSLMLKPLEVVRGRLAQCAPWNRFLPILLSATD 575
QY 535 NIDEAEWEMKAGFHRMKNMMMDKQNDQTSKESCVGL 574
DB 576 TLDEAERQWRAEFHRMSSYVHWKNQPDHY-SKQERCSDL 614

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RESULT 18

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ID BAC31228 PRELIMINARY; PRT; 614 AA.
AC BAC31228;
DT 14-APR-2004 (TREMBlrel. 27, Created)
DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)
DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE clone:A630083607 product:acetylcholinesterase, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,

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RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK042335; BAC31228.1; -
 SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;

Query Match 53.9%; Score 1675.5; DB 2; Length 614;
 Best Local Similarity 52.8%; Pred. No. 2,3e-117; Indels 7; Gaps 4;
 Matches 306; Conservative 104; Mismatches 163;

QY 1 EDDIIATKNGKVRGNMLTVFGTVAFLGIPYAPPLGRLREFKPKQSLTKMSDINATK 60
 Db 36 DPQLVAVRGGQLRGIRLKAPEGVSAFLGIPFAEPVSGRRFMPBPCKPWSGLDAT 95
 QY 61 YANSCCNITQSPFGFSGEMWNPNTLSECLYINWIPAPKPKAT-VLIWYGGGFG 119
 Db 96 FQNVCCYQVDTLVYFGFEGTEWNNRRLSECLYINWTPPRASPLPVLWYGGGFG 155
 QY 120 TGTSSLHYDQKFLARVERVIVSMNRVGAFLGFLPAGNPEAGNGLPQDLATQMVQ 179
 Db 156 SGASLSDVYDRFLAQVGAVALVSMNRVGFGLALPGSREAPGNGLDQRLATQMVQ 215
 QY 180 KNIAFGNPKSVTLTFESAGASVSLHLLSPGSHLFTFRAILIOGSSFNAPWATSLYEA 239
 Db 216 ENIAAFGDPMSVTLTFESAGASVGMHLLSLPERSLFHRAVLQSGTPNGFWATVSA 275
 QY 240 NRRRLNLAQLTGC-----SRENETIICLRKRDQOEILLNAPFVPGTPLSVNPGTVD 295
 Db 276 RRRATYLLARLVGCPGAGGNDTLLICLRPAQDLDVDEHMHVLPQBSIFRESFVVD 335
 QY 296 GDFLTDMPDILLEGOFKTQILVGVNDEGTWFLVYGAPGFSKDNNSITRKEFOGLK 355
 Db 336 GDFLSDPEALINNGDQDLVLGVVDEGSYFLVGVPEFSKDNLSIRAGFLAGVR 395
 QY 356 IFFPGVSEFGKESLFFHTDWDQORPENYBALGDVGVNFCPLAEFKKSEWGN 415
 Db 396 IGVPAASDLAEAVLHTDWMHEDPHTLRDAMSADVGDHNVVCPVAQLAGRLAAGAR 455
 QY 416 AFFFFEHRSKLTPWPMWGMHGEIEFVFGPLERDNTKAEILSRISIVRMNFA 475
 Db 456 VYATIFERRASTLTWPLMWSVPHGEIEFIFGLDPSLNTTERTIRPAQMLKWNINFA 515
 QY 476 KYGNPNNTQNN-STSWPVFKSTQKYLTLNTESTRTIMTKLRAOQCFWTFSPVLENTG 534
 Db 516 RTGPNDRDSDSPQWPPYTTAAQYVSLNKLPLEVRGRLAQAFCANRLPLSLSTD 575
 QY 535 NIDEAEWEMKAGPHRNNYMDWKNQPNDYTSKESCTGL 574
 Db 576 TLDEAEQWKABFRHSSSYVMWKNQFDHY-SKQRCSDL 614

ID BAC31641 PRELIMINARY; PRT; 614 AA.
 AC BAC31641;
 DT 14-APR-2004 (TREMBLrel. 27, Created)
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
 DE 10 days neonate cortex cDNA, RIKEN full-length enriched library,
 DE clone: A830027P05 product: acetylcholinesterase, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573 (2002).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Teshiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RESULT 19
 BAC31641


```

QY 240 RNNLTNLAKITGC-----SRNENETIICLRANKDPOEILNEAFVVPYGTPLSNFGPTVD 295
DB 276 RRRATTLARLVGCPGAGAGNDTELACLRTPAQLVDHEMVLVQESIIFRSEFVAVD 335
QY 296 GDBLTMDPDLLELGGPKTKQIILVGNKDEGTWFLVYAGPFSKDNNSITTRKEFOEGLK 355
DB 336 GDBLTMDPDLLELGGPKTKQIILVGNKDEGTWFLVYAGPFSKDNNSITTRKEFOEGLK 395
QY 356 IFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEWANN 415
DB 396 IGVPGASDLAAEAVVLYHTDMLHPEDPTHLDAMSAYVGDHNVVCPAQLAGRLAAQGAR 455
QY 416 APEYFHHSSSKLPPEWGVGHGYEIEFVGLPLERDNTYTAEEILSSITKRWANPA 475
DB 456 VYAVIPEHRASTLTWPLMGVPHGYEIEFVGLPLERDNTYTAEEILSSITKRWANPA 515
QY 476 KYGNPNPTONN-STSWVFSTKCYLTLNTESTRITKLRACQCFWTSFFPKVLEMTG 534
DB 516 RTGDNDPDRSKSPQWPPYTTAAQYVSLNKLPLEVRGRLAQTCAPWNRFLKLSATD 575
QY 535 NIDEAEWEMKAGFHRNNNMWKNQPNDYTSKXESCVGL 574
DB 576 TLDEAEKQWKAEPFRMGSYVWVMKNQPDHY-SKQERCSDL 614

RESULT 21
QY 09GKJ6 PRELIMINARY; PRT; 349 AA.
AC 09GKJ6;
DT 01-MAR-2001 (TREMBLER, 16, Created)
DT 01-MAR-2001 (TREMBLER, 16, Last sequence update)
DT 01-OCT-2003 (TREMBLER, 25, Last annotation update)
DE Butyrylcholinesterase (fragment).
GN Name=ACHE;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419000; PubMed=11528129;
RA Van Poucke M., Yexle M., Tuggle C., Piumi F., Genet C.,
RA Van Zeveren A., Peelman L.J.;
RT "Integration of porcine chromosome 13 maps.";
CC Cytochrome C11 gene. 93:297-303(2001).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DB EMBL; AF222914; AAC41127.1;
DB GO; GO:0003824; F:catalytic activity; IEA.
DB GO; GO:0004104; F:cholinesterase activity; IEA.
DB InterPro; IPR002018; Cholinesterase.
DB InterPro; IPR000997; Cholinesterase.
DB InterPro; IPR000379; Ser_estrs.
DB Pfam; PF00135; Coesterase; 1.
DB PRINTS; PR00878; CHOLINESTERASE.
DB PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
FT NON_TER 1
FT NON_TER 349
SQ SEQUENCE 349 AA; 39061 MW; D66354B14725B58 CRC64;

Query Match 53.8%; Score 1674; DB 2; Length 349;
Best Local Similarity 91.4%; Pred. No. 1,4e-117;
Matches 319; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

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DB 121 VTSLYEARNRTLAKIFGCSRENETIICLRANKDPOEILQNEFVVPNNHLLSVNGP 180
QY 232 TYDGFRLMDPDLLELGGPKTKQIILVGNKDEGTWFLVYAGPFSKDNNSITTRKEFOE 352
DB 181 TYDGFRLMDPDLLELGGPKTKQIILVGNKDEGTWFLVYAGPFSKDNNSITTRKEFOE 240
QY 353 GLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEW 412
DB 241 GLKIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYNFICPALEFTKFSSEW 300
QY 413 GNNAFYFHHSSSKLPPEWGVGHGYEIEFVGLPLERDNTYTAEEILSSITKRWANPA 461
DB 301 GNNAFYFHHSSSKLPPEWGVGHGYEIEFVGLPLERDNTYTAEEILSSITKRWANPA 349

RESULT 22
ACCS FELCA STANDARD; PRT; 611 AA.
ID ACES_FELCA
AC 062763; 062762;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=20334351; PubMed=10874122;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma.";
RL Biochem. Pharmacol. 60:479-487(2000).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC required to anchor it to the basal lamina of cells and organized
CC into tetramers (By similarity). Isoform H generates multiple structures,
CC dimers; disulfide linked. Isoform T generates multiple structures,
CC ranging from monomers and dimers to collagen-tailed and
CC hydrophobic-tailed forms, in which catalytic tetramers are
CC associated with anchoring proteins that attach them to the basal
CC lamina or to cell membranes. In the collagen-tailed forms, isoform
CC T subunits are associated with a specific collagen, COLQ, which
CC triggers the formation of isoform T tetramers, from monomers and
CC dimers.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=T;
CC IsoId=O62763-1; Sequence=displayed;
CC Name=H;
CC IsoId=O62763-2; Sequence=VSP_001456;
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to jlicene@sib-sib.ch).
DB EMBL; AF053485; AAC08995.1;
DB EMBL; AF053485; AAC08996.1;
DB HSSP; P22303; 1F8U.
DB InterPro; IPR002018; Cholinesterase.
DB InterPro; IPR000997; Cholinesterase.
DB InterPro; IPR000379; Ser_estrs.
DB Pfam; PF00135; Coesterase; 1.

```


[illegible]

Search completed: January 6, 2005, 09:59:42
Job time : 203 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 09:50:36 ; Search time 43 Seconds
(without alignments)
1284.382 Million cell updates/sec

Title: US-09-748-739a-2_COPY_29_602
Perfect score: 3110
Sequence: 1 EDDIIITATKNGKVRGNMLTV.....MDMKNPNDYTSKESCVGL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3096	99.5	602	1	ACHU
2	2843	91.4	581	2	cholinesterase (EC
3	2521	81.1	603	2	cholinesterase (EC
4	1785.5	57.4	596	1	acetylcholinesterase (EC
5	1784.5	57.4	599	1	acetylcholinesterase (EC
6	1689	54.3	614	2	acetylcholinesterase (EC
7	1678.5	54.0	614	2	acetylcholinesterase (EC
8	1675.5	53.9	614	2	acetylcholinesterase (EC
9	1639	52.7	584	2	acetylcholinesterase (EC
10	1636.5	52.6	583	2	acetylcholinesterase (EC
11	1455.5	46.8	767	2	acetylcholinesterase (EC
12	1142	36.7	620	2	acetylcholinesterase (EC
13	1070.5	34.4	637	2	acetylcholinesterase (EC
14	1044	33.6	746	2	acetylcholinesterase (EC
15	1040.5	33.5	691	2	acetylcholinesterase (EC
16	1030.5	33.1	664	2	acetylcholinesterase (EC
17	1012.5	32.6	602	2	acetylcholinesterase (EC
18	948	30.5	629	2	acetylcholinesterase (EC
19	937	30.1	629	2	acetylcholinesterase (EC
20	930	29.9	607	2	acetylcholinesterase (EC
21	893	28.7	532	2	acetylcholinesterase (EC
22	754	24.2	532	2	acetylcholinesterase (EC
23	732	23.5	599	2	acetylcholinesterase (EC
24	729	23.4	597	2	acetylcholinesterase (EC
25	728.5	23.4	559	1	carboxylesterase (E
26	726	23.3	612	2	carboxylesterase (E
27	724	23.3	141	2	cholinesterase (EC
28	721	23.2	141	2	cholinesterase (EC

30	721	23.2	141	2	B39768	cholinesterase (EC
31	718.5	23.1	561	2	S47655	carboxylesterase (E
32	715	23.0	554	2	A39060	carboxylesterase (E
33	711	22.9	745	2	S13586	triacylglycerol 11
34	708.5	22.8	565	2	S10367	carboxylesterase (E
35	707	22.7	141	2	B39768	cholinesterase (EC
36	701.5	22.6	557	2	A47162	cholinesterase B (E
37	697.5	22.4	567	1	A41010	carboxylesterase (E
38	696.5	22.4	562	2	A55281	carboxylesterase (E
39	694.5	22.3	561	2	JC2447	carboxylesterase (E
40	690.5	22.2	566	2	S19307	carboxylesterase (E
41	690	22.2	549	2	JX0054	carboxylesterase (E
42	689	22.2	540	2	A31584	carboxylesterase (E
43	680.5	21.9	561	2	S62788	carboxylesterase (E
44	675.5	21.7	561	2	S71597	carboxylesterase (E
45	666	21.4	956	2	A56920	glucocorticoid precurs
46	651	20.9	554	1	S34607	carboxylesterase (E
47	649	20.9	540	2	S51043	carboxylesterase (E
48	634	20.4	2769	1	UIBO	thyroglobulin prec
49	631	20.3	967	1	UIRT	thyroglobulin - ra
50	627	20.2	540	2	A75250	carboxylesterase (E
51	623.5	20.0	593	1	S25062	triacylglycerol 11
52	619	19.9	539	2	A29923	carboxylesterase (E
53	614	19.4	2767	1	UIHU	thyroglobulin prec
54	603.5	19.4	562	2	S27782	esterase precursor
55	595	19.1	564	1	S36787	carboxylesterase (E
56	594	19.1	489	2	B69680	para-nitrobenzyl e
57	585.5	18.8	506	2	T25690	hypothetical prote
58	585	18.8	506	2	H75522	probable carboxyle
59	583	18.7	552	2	S36786	carboxylesterase (E
60	582.5	18.7	554	2	T31783	hypothetical prote
61	582.5	18.7	557	2	A56690	esterase - Caenorh
62	574.5	18.5	564	2	T28949	hypothetical prote
63	556	17.9	547	2	T29717	hypothetical prote
64	554.5	17.8	562	2	S27800	elastase precursor
65	553	17.6	548	2	T32907	hypothetical prote
66	546.5	17.6	550	1	A34576	cysteal protein pr
67	540.5	17.4	570	2	T32061	gut-specific carbo
68	538.5	17.3	730	2	T16455	hypothetical prote
69	531.5	17.1	502	2	AE0666	probable esterase
70	528.5	17.0	578	2	P89068	protein T28C12.4b
71	528.5	17.0	658	2	T32053	hypothetical prote
72	526	16.9	543	2	T27000	hypothetical prote
73	522	16.9	565	2	T29718	protein B0238.1 (I
74	520.5	16.7	545	2	A89046	esterase B1 - sout
75	520	16.7	540	2	A35986	carboxylesterase (E
76	512	16.5	540	2	S53371	protein K07C11.4 (
77	510	16.4	571	2	G89123	hypothetical prote
78	509.5	16.4	798	2	T19864	carboxylesterase (E
79	508	16.3	540	2	S53370	D2 protein precurs
80	507	16.3	535	2	B34576	protein B0238.7 (I
81	499.5	16.1	549	2	B89045	triacylglycerol 11
82	497	16.0	578	2	UN0552	triacylglycerol 11
83	491	15.8	453	2	G89045	protein B0238.2 (I
84	482.5	15.5	544	2	A34325	juvenile-hormone e
85	482	15.5	544	2	A41094	triacylglycerol 11
86	481	15.5	563	1	PN0493	triacylglycerol 11
87	479	15.4	544	2	A41095	triacylglycerol 11
88	477	15.3	548	2	S32615	triacylglycerol 11
89	476	15.3	544	2	A41096	triacylglycerol 11
90	476	15.3	544	2	S41093	triacylglycerol 11
91	474	15.2	544	2	B34089	carboxylesterase (E
92	473	15.2	544	2	B40122	carboxylesterase (E
93	473	15.2	544	2	A41426	carboxylesterase (E
94	473	15.2	544	2	A34089	carboxylesterase (E
95	473	15.2	548	2	A28022	carboxylesterase (E
96	472	15.2	544	2	C41426	carboxylesterase (E
97	471.5	15.2	563	2	S59957	triacylglycerol 11
98	470	15.1	544	2	S59958	triacylglycerol 11
99	468	15.0	544	2	D41426	carboxylesterase (E
100	468	15.0	544	2	I41426	carboxylesterase (E

Qy 2 DDIITATKNGKVGKMLTVFGGTVTAFLGIPYAOPPLGRLRFPKPKQSLTKMSDIMNATK 61
 Db 9 EDVLIITTKNGRIRGINLPVFGGTATFAGIPYAOPPLGRLRFPKPKQSLTKMSDIMNATK 68
 Qy 62 ANSCCONIDQSPFGHSEMMNPNTDLSDDCLYLNWIPAKPKKNAITVLIWYGGFQ 121
 Db 69 ANSCCONIDQSPFGHSEMMNPNTDLSDDCLYLNWIPAKPKKNAITVLIWYGGFQ 128
 Qy 122 TSSLAHYDQKFLARVERIVVSNMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 181
 Db 129 TSSLAHYDQKFLARVERIVVSNMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 188
 Qy 182 IAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFWATVSLYEARN 241
 Db 189 IAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFWATVSLYEARN 248
 Qy 242 RTLNLAKLTGCSRENETEIKCLRNKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 301
 Db 249 RTLNLAKLTGCSRENETEIKCLRNKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 308
 Qy 302 MPDILLELQGFKQTLVGNKDEGTWFLVYAGAPGFSKONNSITTRKEFOEGKIFPPGV 361
 Db 309 MPDILLELQGFKQTLVGNKDEGTWFLVYAGAPGFSKONNSITTRKEFOEGKIFPPGV 368
 Qy 362 SEFGKESILFHYTDWDDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 421
 Db 369 SEFGKESILFHYTDWDDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 428
 Qy 422 EHRSSKLPWPMWGVNMGHGEIEFVFGPLERRDNTYKAEILSRIVKMANPAKYGNP 481
 Db 429 EHRSSKLPWPMWGVNMGHGEIEFVFGPLERRDNTYKAEILSRIVKMANPAKYGNP 488
 Qy 482 ETONNSTWMPVKSTBOXYLTNTTESTRIMTKLRAPQOCRFWTSFPKYLEMTGNIDEAE 541
 Db 489 ETONNSTWMPVKSTBOXYLTNTTESTRIMTKLRAPQOCRFWTSFPKYLEMTGNIDEAE 548
 Qy 542 EMKAGFHRMNNYMDWKQFNQNDYTSKKESCVG 573
 Db 549 EMKAGFHRMNNYMDWKQFNQNDYTSKKESCVG 580

RESULT 3
 S70849
 N:Alternate names: butyrylcholine esterase
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Oct-1996 #sequence revision 08-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S70849; S15680; A39768
 R:Taylor, P.
 submitted to the EMBL Data Library, August 1992
 A:Reference number: S70849
 A:Accession: S70849
 A:Molecule type: nucleic acid
 A:Residues: 1-603 <TRY>
 A:Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:q191579; PIDN:AAA37328.1; PID:q1915
 R:Schumacher, M.; Camp, S.; Li, Y.; Ekstrom, T.J.; Newton, M.; Taylor, P.
 Neuron 5, 317-327, 1990
 A>Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
 A:Reference number: JH0314; MUID:90380429; PMID:2400605
 A:Accession: S15680
 A:Molecule type: nucleic acid
 A:Residues: 30-128, 'P', 130-603 <RAC>
 A:Cross-references: EMBL:M99492
 R:Apagana, M.; Chalmers, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
 J. Biol. Chem. 266, 6966-6974, 1991
 A>Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
 A:Reference number: A39768; MUID:91201348; PMID:2016308
 A:Accession: A39768
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 97-128, 'P', 130-237 <ARP>

C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:57-557/Domain: cholinesterase homology <CHB>

Query Match 81.1%; Score 2521; DB 2; Length 603;
 Best Local Similarity 80.5%; Pred. No. 3.5e-185;
 Matches 462; Conservative 47; Mismatches 65; Indels 0; Gaps 0;

Qy 1 EDDIITATKNGKVGKMLTVFGGTVTAFLGIPYAOPPLGRLRFPKPKQSLTKMSDIMNATK 60
 Db 30 EDDIITATKNGRIRGINLPVFGGTATFAGIPYAOPPLGRLRFPKPKQSLTKMSDIMNATK 89
 Qy 61 YANSCCONIDQSPFGHSEMMNPNTDLSDDCLYLNWIPAKPKKNAITVLIWYGGFQ 120
 Db 90 YANSCCONIDQSPFGHSEMMNPNTDLSDDCLYLNWIPAKPKKNAITVLIWYGGFQ 149
 Qy 121 GTSSLHYDQKFLARVERIVVSNMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180
 Db 150 GTSSLHYDQKFLARVERIVVSNMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 209
 Qy 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFWATVSLYEARN 240
 Db 210 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAFWATVSLYEARN 269
 Qy 241 NRTNLAKLTGCSRENETEIKCLRNKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
 Db 270 NRTNLAKLTGCSRENETEIKCLRNKDPQOILLNEAFVVPYGTPLSVNFGPTVDGDFLT 329
 Qy 301 MPDILLELQGFKQTLVGNKDEGTWFLVYAGAPGFSKONNSITTRKEFOEGKIFPPGV 360
 Db 330 MPDILLELQGFKQTLVGNKDEGTWFLVYAGAPGFSKONNSITTRKEFOEGKIFPPGV 389
 Qy 361 VSEFGKESILFHYTDWDDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 420
 Db 390 VSEFGKESILFHYTDWDDQRENTREALGDVVDYVFCPALFETKCFSEMGNAFFYYF 449
 Qy 421 EHRSSKLPWPMWGVNMGHGEIEFVFGPLERRDNTYKAEILSRIVKMANPAKYGNP 480
 Db 450 EHRSSKLPWPMWGVNMGHGEIEFVFGPLERRDNTYKAEILSRIVKMANPAKYGNP 509
 Qy 481 NETONNSTWMPVKSTBOXYLTNTTESTRIMTKLRAPQOCRFWTSFPKYLEMTGNIDEAE 540
 Db 510 NETONNSTWMPVKSTBOXYLTNTTESTRIMTKLRAPQOCRFWTSFPKYLEMTGNIDEAE 569
 Qy 541 EMKAGFHRMNNYMDWKQFNQNDYTSKKESCVG 574
 Db 570 EMKAGFHRMNNYMDWKQFNQNDYTSKKESCVG 603

RESULT 4
 ACRYE
 acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric ray
 N:Alternate names: acetylcholinesterase, asymmetric form
 C:Species: Torpedo californica (Pacific electric ray)
 C>Date: 17-Mar-1987 #sequence revision 08-Nov-1996 #text_change 09-Jul-2004
 C/Accession: A00773; A60820; B31962; A23902; B4117; S15677
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macpherson-Guigley, K.; Taylor, S.S.; F
 Nature 319, 407-409, 1986
 A>Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its c
 A:Reference number: A00773; MUID:86118676; PMID:3753747
 A:Accession: A00773
 A:Molecule type: mRNA
 A:Residues: 'NS', 11-596 <SGH>
 A:Cross-references: UNIPROT:P04058; GB:X03439; NID:g64389
 A:Experimental source: electric organ
 A>Note: parts of this sequence, including the amino and carboxyl ends of the mature prote
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macpherson-Guigley, K.; Taylor, S.S.; F
 Fed. Proc. 45, 2976-2981, 1986
 A>Title: Primary structure of acetylcholinesterase: implications for regulation and funct
 A:Reference number: A60820; MUID:87054662; PMID:3536598
 A:Accession: A60820
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 526-599 <SI2>
 A:Cross-references: EMBL:X13172; NID:964416; PIDN:CA31570.1; PID:964417
 A:Experimental source: clone pACH2
 R:Bon, S.; Chang, J.Y.; Strosberg, A.D.
 FEBS Lett. 209, 206-212, 1986
 A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-soluble acetylcholinesterase.
 A:Reference number: A91370; MUID:87080761; PMID:3792544
 A:Accession: A25650
 A:Molecule type: protein
 A:Residues: 25-40, 'G', 42-47 <BON>
 C:Genetics:
 A:Gene: AChE
 C:Function:
 A:Description: hydrolyzes acetylcholine to choline and acetate
 A:Pathway: neurotransmitter degradation
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter
 F:1-24/DNA: signal sequence #status predicted <SIG>
 F:25-599/Product: acetylcholinesterase #status predicted <MAT>
 F:54-559/DNA: cholinesterase homology <CH>
 F:63,440,481,557/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:91-118,278-289,426-545/Disulfide bonds: #status predicted
 F:224,351,464/Active site: Ser, Glu, His #status predicted
 F:596/Disulfide bonds: interchain #status predicted

Query Match 57.4%; Score 1784.5; DB 1; Length 599;
 Best Local Similarity 53.8%; Pred. No. 1e-128; Indels 1; Gaps 1;
 Matches 309; Conservative 111; Mismatches 153;

1 EDDIIITKNGKRGKMGNTLVFGGTVTAFLGIPYAPAPPLGRLFRKPKQSLTKMSDINWATK 60
 27 DSELVIVTKSGKMTKRTPIPLSSHISAFGLPFAEPVGMRRPRPKPKMGSVWMAST 86
 61 YANSCCONIDQSPFGHSGEMNPNNTDSEDCLYLWVWPAKPKKAT-VLIWYGGF 120
 87 YPNNCOQYVDEQPPGFGSEMNPNRMSHEDCLINIWVSPRKSATVMIWYGGFYS 146
 121 GTSILHYDGKFLARVERVIVSMNRYVAGLGPLALGPNPAGNMGLPQOALALQWVK 180
 147 GSSTLDVYNKTYLTYEEVVLVSIVYVAGFGLALHSGASAPGNMGLDQRLALQWHD 206
 181 NIAFGNPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAPWAVTSLYE 240
 207 NIGFPGDPRKTVTLFGESAGASVGMHLSFGSDLRRAILQSGSPNCMAVSVAEGR 266
 241 NRTLNTAKLTGCSRENTEIILKLRNKPQOILINAEFVVPYGTPLSVNFGPTVDGFLT 300
 267 RRAVELLRNINCNLNSDEDLIQCLREKKPOLLDVENWVLPFDSIFRFSFVVIDGEFFP 326
 301 DMEIDLLELQFKKTOILVGNKDEGWFLVYGA RGSKDNNSITTEKEFOEGLKIFPG 360
 327 TSLSEMLNANPKTKQILLGVNKGSGFPFLYGA RGSKDESKISREDFMGVKSVP 386
 361 VSEFGKESILFHYTDWVDORPENYRALGDVYNFICPALFETKFKSEMGNAFFY 420
 387 ANDLGDAVTLQTTDMDDNNNGIKNRDGLDVIDGHHVIGCPMFVAKYTKFGNGTYLYF 446
 447 FNRASNLVPEWVGVIHGEIEFVGLPLVKEILNTYAEBSALSRRIIMHWATPAKGNP 506
 481 NEQNNSSTPVPFVSTQKTLTNTSTRITMTKLRQOGRFWSFFPKVLEMTGNIDAE 540
 507 NEPSQSKWPLFTTKQKIDLNTTEPIKYHQLRLVQWCVFWNQLPKLNTAETIDEAE 566
 541 MEWKAGFRHNNYMDKQNFNDYTSKESCVGL 574
 567 ROKTEFRHNSSYMHHKNOFDQY-SRHENCAEL 599

RESULT 6
 A39256

acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
 C:Species: Homo sapiens (man)
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
 C:Accession: A39256; S03959
 R:Scored: H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnat, A.; Neville, L.; Lieman-Hurw; Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
 A:Title: Molecular cloning and construction of the coding region for human acetylcholinesterase.
 A:Reference number: A39256; MUID:91088577; PMID:2263619
 A:Accession: A39256
 A:Molecule type: mRNA; DNA
 A:Residues: 1-614 <SOR>
 A:Cross-references: UNIPROT:P22303; GB:M55040; NID:9177974; PIDN:AAA6815.1; PID:9177975
 A:Note: this sequence represents composite of clones including clone ABGACHE from adult brain; should represent an authentic brain splice form
 R:Chajland, V.; Derr, D.; Earles, B.; Schwell, E.; August, T.
 FEBS Lett. 247, 279-282, 1989
 A:Title: Purification and partial amino acid sequence analysis of human erythrocyte acetylcholinesterase.
 A:Reference number: S03959; MUID:89232136; PMID:2714437
 A:Accession: S03959
 A:Molecule type: protein
 A:Residues: 256-266, 'Y', 268-273; 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-326, 'Y', 532-551 <CH>
 A:Experimental source: erythrocytes
 A:Note: this form was a disulfide-linked homodimer
 C:Genetics:
 A:Gene: GDB:ACH; YT
 A:Cross-references: GDB:118746; OMIM:100740
 A:Map position: 7q22-7q22
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidylcholine
 F:63-569/DNA: cholinesterase homology <CH>

Query Match 54.3%; Score 1689; DB 2; Length 614;
 Best Local Similarity 52.8%; Pred. No. 2.2e-121; Indels 8; Gaps 5;
 Matches 307; Conservative 104; Mismatches 162;

1 ED-DIIATKNGKRGKMGNTLVFGGTVTAFLGIPYAPAPPLGRLFRKPKQSLTKMSDINWATK 59
 35 EDDELIVTVAGRLRKLTKPGSPVSAFLGIFAEPPMGRFLPEPQPMGVDAT 94
 60 KYANSCCONIDQSPFGHSGEMNPNNTDSEDCLYLWVWPAKPKKAT-VLIWYGGF 118
 95 TFSQVCQYVDTLYPFGEGTEMNPNRRELSHEDCLYLNWVWPAKPKKAT-VLIWYGGF 154
 119 QGTSSILHYDGKFLARVERVIVSMNRYVAGLGPLALGPNPAGNMGLDQRLALQW 178
 155 YGASSLDVYDGFLLVQAKRTVIVSMNRYVAGLGPLALGPNPAGNMGLDQRLALQW 214
 179 QKNIAAFGKNSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAPWAVTSLYE 238
 215 QENVAAFGDPRKTVTLFGESAGAASVGMHLSFGSDLRRAILQSGSPNCMAVSVAEGR 274
 239 ARNRTNLAKLTGCSRENTEIILKLRNKPQOILINAEFVVPYGTPLSVNFGPTV 294
 275 ARRAATQALVLCPPGCTGNDTELVACLRTPAQVTVNHEHNVLPQESVFRFSFV 334
 295 DGEFLDMDLLELQFKKTOILVGNKDEGWFLVYGA RGSKDNNSITTEKEFOEGL 354
 335 DGEFLDMDLLELQFKKTOILVGNKDEGWFLVYGA RGSKDNNSITTEKEFOEGL 394
 355 KIFPGVSEFGKESILFHYTDWVDORPENYRALGDVYNFICPALFETKFKSEMGNAFFY 414
 395 RGVGPVQSDLAALAVLHLYDMHPEDPARLRALSDVGDHNVICPVQDLAORLAQGA 454
 415 NAEFYFHEHSSKLPMPWEMGVNGHYIEFVGLPLERDNYTKAEIISRSIVKMANF 474
 455 RYVAAYVEHRASTSLPMLMVGPHGEIEFVGLPLERDNYTKAEIISRSIVKMANF 514
 475 AKYGNPENTON-NSTMPVPSKTEQKTLTNTSTRITMTKLRQOGRFWSFFPKVLEMT 533
 515 AKTGDPNEPRDPPAPPPYTAGAQVSDLRPLEVRKGLRQACAFNRFLPKLSAT 574
 534 GNIDEAEWEMKAGFRHNNYMDKQNFNDYTSKESCVGL 574

C;Species: *Oryctolagus cuniculus* (domestic rabbit)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
C;Accession: S48724
R;Jllo, O.; L'Hermite, Y.; Talea, V.; Tourant, J.P.; Chalonnet, A.
Eur. J. Biochem. 225, 115-124, 1994
A;Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue
A;Reference number: S48724; MUID:95010096; PMID:7925428
A;Accession: S48724
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-584 <JBI>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: glycoprotein
F;32-539/Domain: cholinesterase homology <CHE>

Query Match 52.7%; Score 1639; DB 2; Length 584;
Best Local Similarity 51.5%; Pred. No. 1.4e-117;
Matches 299; Conservative 106; Mismatches 168; Indels 8; Gaps 5;

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QY 1 EDIIITKNGKVGKMLTVFGTAVTAFLGIPYAPPLGRLFRKPKQSLTKMSDINATK 60
D 5 DEPLVAVRGGRGLRLKAPGVSAFLGIFPEEPGRPLPPEPKRMAVLATA 64
QY 61 YANSCCNIDSPFGFSGEMNPNTDISEDCLYLVNWIAPKPKNAT-VLIMYGGGFQ 119
D 65 FQGVGYVDTLVYGFEGTEMMNPNRLSEDCLYLVNWTYPKPSPTPLVIMYGGGFY 124
QY 120 TGTSSLHVDGKFLARVERIVVSM-NYRVGALGFLALPGNPEAPGNMGLFDQALALQW 178
D 125 SGASSLDLYVYGRFLVQAEGLVAMHVRVGAFFGFTCLPGSREAPGNVGLDQRLALQW 184
QY 179 QKNIATFGNPKSVTLFGESAGASVSLHLSPGSHSLFTPAIIQSOSFNAPMAVTSLEYE 238
D 185 QENVAARCGBPASVTLFGESAGASVGLHLSPPSRGLFHRVAVLQSGAPNPMATVGE 244
QY 239 ARNETLNLAKLTGC---SRENTEIILKLNKDPQBITLNEAFVVPYGPPLSVNFGPTV 294
D 245 ARRAATLILARLVNCPGAGAGNDTELVACLRPAQDLVDHEMRVLPOESIFRSFVAV 304
QY 295 DGDPLTMDPDLLELGGPKTKQIILVGNKDEGTWFLVYGAFSGKDNNSITTRKEFOGLK 354
D 305 DGDPLSTPEALINAGFVGLQVAVGVKDEGTWFLVYGAFSGKDNNSITTRKEFOGLK 364
QY 355 KIFPGVSEFKESILFHYTMDVDQRPENRREALGVDVGNFICPALBETKKESEWGN 414
D 365 RVGVPQASDLAAEAVLHYTMDLHPEDPARLRLSDVDGHNVCVPAQLAGLAAQGA 424
QY 415 NAFYFEHRSKSLPPEMGMVMEGYEIEFVGLPLERDNYTKAEILSRISYRWANF 474
D 425 RVAVYVEHRASTLSWPLMGVPHGYEIEFIFGLPLBSLNTYTBERRIPARLRYWANF 484
QY 475 AKYGNPNETO-NSTSWPVEKSTQKYLTLNTBSTRIMTKLRAQOCRFWISFPKVLMTG 533
D 485 ARGTDPNPPAPKAPQWPPYTAGAQVYVSLNRLPLGVQASRAQACAFWNRFLPKLNSAT 544
QY 534 GNIDEAEMEKAGFHRNNVMMDKNOFNDTSKKESCVGL 574
D 545 DTLDARQWAFBHRWSYVHWKNDYH-SKQDRCSL 584
```

RESULT 10

101072
acetylcholinesterase (EC 3.1.1.7) - bovine
C;Species: *Bos primigenius taurus* (cattle)
C;Date: 21-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 12-May-1995
C;Accession: S10712; A39734; B39734; B25650
R;Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K.
FEBS Lett. 266, 123-127, 1990
A;Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its
A;Reference number: S10712; MUID:90306335; PMID:2365060
A;Accession: S10712
A;Molecule type: protein
A;Residues: 1-583 <DOC>

A;Experimental source: fetal serum
R;Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.
J. Biol. Chem. 266, 7481-7487, 1991
A;Title: Bovine brain acetylcholinesterase primary sequence involved in interubunit dis
A;Reference number: A39734; MUID:91210255; PMID:2019579
A;Accession: A39734
A;Molecule type: protein
A;Residues: 1-15, 'R', 17-38, 225-235, 'X', 237-244, 248-264, 'X', 266-273, 365-380, 396-404, 'X', 4
A;Experimental source: brain, erythrocyte
A;Accession: B39734
A;Molecule type: protein
A;Residues: 1-38 <RQZ>
A;Experimental source: fetal serum
R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solub
inesterase.
A;Reference number: A91370; MUID:87080761; PMID:3792544
A;Accession: B25650
A;Molecule type: protein
A;Residues: 'XS', 3-12 <BN>
A;Experimental source: caudate nucleus
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;32-536/Domain: cholinesterase homology <CHE>
F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Active site: Ser #status predicted

Query Match 52.6%; Score 1636.5; DB 2; Length 583;
Best Local Similarity 51.7%; Pred. No. 2.1e-117;
Matches 300; Conservative 103; Mismatches 170; Indels 7; Gaps 4;

```
QY 1 EDIIITKNGKVGKMLTVFGTAVTAFLGIPYAPPLGRLFRKPKQSLTKMSDINATK 60
D 5 DEPLVAVRGGRGLRLKAPGVSAFLGIFPEEPGRPLPPEPKRMAVLATA 64
QY 61 YANSCCNIDSPFGFSGEMNPNTDISEDCLYLVNWIAPKPKNAT-VLIMYGGGFQ 119
D 65 FQGVGYVDTLVYGFEGTEMMNPNRLSEDCLYLVNWTYPKPSPTPLVIMYGGGFY 124
QY 120 TGTSSLHVDGKFLARVERIVVSMNYRVGALGFLALPGNPEAPGNMGLFDQALALQW 179
D 125 SGASSLDLYVYGRFLVQAEGLVAMHVRVGAFFGFTCLPGSREAPGNVGLDQRLALQW 184
QY 180 KNIATFGNPKSVTLFGESAGASVSLHLSPGSHSLFTPAIIQSOSFNAPMAVTSLEYE 239
D 185 ENVAARCGDPTSVTLFGESAGASVGLHLSPPSRGLFHRVAVLQSGAPNPMATVGEA 244
QY 240 RNRITLNLAKLTGC---SRENTEIILKLNKDPQBITLNEAFVVPYGPPLSVNFGPTVD 295
D 245 RRAATLILARLVNCPGAGAGNDTELVACLRPAQDLVDHEMRVLPOEHRFRSFPVAV 304
QY 295 DGDPLTMDPDLLELGGPKTKQIILVGNKDEGTWFLVYGAFSGKDNNSITTRKEFOGLK 355
D 305 DGDPLSTPEALINAGFVGLQVAVGVKDEGSFVLYGAFSGKDNNSITTRKEFOGLK 364
QY 355 IFFPGVSEFKESILFHYTMDVDQRPENRREALGVDVGNFICPALBETKKESEWGN 415
D 365 VGVQASDLAAEAVLHYTMDLHPEDPARLRLSDVDGHNVCVPAQLAGLAAQGA 424
QY 416 AIFYFEHRSKSLPPEMGMVMEGYEIEFVGLPLERDNYTKAEILSRISYRWANF 475
D 425 VVAVYVEHRASTLSWPLMGVPHGYEIEFIFGLPLBSLNTYTBERRIPARLRYWANF 484
QY 476 KYGNPNETO-NSTSWPVEKSTQKYLTLNTBSTRIMTKLRAQOCRFWISFPKVLMTG 534
D 485 RTDPPNPPAPKAPQWPPYTAGAQVYVSLNRLPLGVQASRAQACAFWNRFLPKLNSAT 544
QY 535 NIDEAEMEKAGFHRNNVMMDKNOFNDTSKKESCVGL 574
D 545 TLDEARQWAFBHRWSYVHWKNDYH-SKQDRCSL 583
```


Qy 530 LEMTGNIDEAEWKGAFHRW-NNYMADWKNQFNQDY-----TSKKECVG 573
 Db 569 MAADVADGDPYLWVKQMDKQNEIYITDQWHEFYKRYQYTRSDSETGG 620

RESULT 13

S66236
 acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito
 C:Species: Aedes aegypti (yellow fever mosquito)
 C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S66236
 R:Anthony, N.; Rocheleau, T.; Mocolin, G.; Lee, H.-J.; ffrench-Constant, R.
 FEBS Lett. 368, 461-465, 1995
 A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene
 A:Reference number: S66236; MUID:95361924; PMID:7635199
 A/Accession: S66236
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-637 <ANT>
 A:Cross-references: UNIPROT:Q9TX11
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-637/Product: acetylcholinesterase #status predicted <MAT>
 F:57-594/Domain: cholinesterase homology <CHE>

Query Match 34.4%; Score 1070.5; DB 2; Length 637;
 Best Local Similarity 38.9%; Pred. No. 6e-74; Mismatches 207; Indels 53; Gaps 8;
 Matches 223; Conservative 90;

Qy 2 DDIITATKNGKVGKGNMLTVFGGTVTAFLGIPYAOPLGRLFRKKQSLTKMSIDIMATKY 61
 Db 31 DRIVVQSSGPGRKRSIMVLGRVHVNQVPAKRPVDSGRFRKFPVAEPMHGVLDATRL 90
 Qy 62 ANSCCNIDSPFGFSGSEMMNPNTDISEDCLYINWIPAP----- 101
 Db 91 PSCIGREYEPFGFAGEEMWNPNTVSEDCLYINWIPKTRLRHGRGLFGNNDYFOD 150
 Qy 102 -----PKPKATVLIWIYGGFQGTSSLHYVDGKFLARVERIVVSMNRYVALGF 153
 Db 151 DDDFQRHQSGKGLAMLVWYIGGGFMSGTSLDLYNEMLAAGNVIVASMQYKVGSGFG 210
 Qy 154 LALP---GNPEAPGNMGLPQOOLALQWOKNIAAFGNGPKSVTLFGESAGASVSLHLS 210
 Db 211 FYLAPYLNDDAEGNVGLMDALAIRWIKENAKAFSGDPDLITLFGESAGSSVSLHLS 270
 Qy 211 PGSHSLFTRAILQSGSFNAPMAVTSLYEARNRTLNLAKLTGCS-----RENETELIKLAR 266
 Db 271 PVTRGASRRGILQGLTINAPMSHSAEKALSVAAALIDDCNCVTLTKDNPVYMNCMRN 330
 Qy 267 KDPQELLINAEFVVPYPTPLSVNFGPTVVDGFLTMDLILBLGQFKTQILVANKDEG 326
 Db 331 VDAKTSIVQO--WNSYSGILGFPSPAPITDGVMTADMTMLREANLGEVLELWGSNDEG 388
 Qy 327 TWPLFVNG-APGFSKDNNSIITRKEFOGLKIFPPGVSEFGKESILFHYTMVDQRENY 385
 Db 389 TYPLFDPIFYFEKDAATSLPRDKFLIEMWTIFSKASPEREALITFQYTGESANDQYON 448
 Qy 386 REALGVVGVNFCPALFEFTKFSSEWGNNAFFYYFHEHRSKLPWPMGMVMSYLEFV 445
 Db 449 QQQQGRSGVGHFFICPTNEFALGLAERGASVYVYVYFTHRTSTSLMGEMGVLDDEVEXI 508
 Qy 446 FGLPLERRDNYTKAEELLSRSIVKMANPAKYGNPNETONNSTSWPVFKSTEQKIYTLANT 505
 Db 509 FGQPMNVSMQYRQREBLDSRMVLSVEFARSQNP--ALEGEHVPYTYKENPIYTFENA 565
 Qy 506 ESTRIWTKLRQO-----GPFWTSPPPKV 529
 Db 566 EGE---DDLNGEKYGRGPMAATACAFMDFLPR 595

RESULT 14

A25363
 acetylcholinesterase (EC 3.1.1.7) precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 16-Aug-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: A25363; A33469
 R:Hall, L.M.C.; Splerer, P.
 EMBO J. 5, 2949-2954, 1986
 A:Title: The Aa locus of Drosophila melanogaster: structural gene for acetylcholinesterase
 A:Reference number: A25363; MUID:87080281; PMID:3024971
 A/Accession: A25363
 A:Molecule type: mRNA
 A:Residues: 1-746 <HML>
 A:Cross-references: UNIPROT:P07140
 A:Note: the authors translated the codon TGG for residue 18 as Cys and AGA for residue 27.
 R:Fournier, D.; Karch, F.; Bride, J.M.; Hall, L.M.C.; Berge, J.B.; Splerer, P.
 J. Mol. Biol. 210, 15-22, 1989
 A:Title: Drosophila melanogaster acetylcholinesterase gene structure, evolution and mutati
 A:Reference number: A33469; MUID:9064544; PMID:2511327
 A/Accession: A33469
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 98-746 <FOU>
 A:Cross-references: GB:X17572
 C:Genetics:
 A:Gene: FlyBase: Ace
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:164-704/Domain: cholinesterase homology <CHE>

Query Match 33.6%; Score 1044; DB 2; Length 746;
 Best Local Similarity 37.9%; Pred. No. 8.2e-72;
 Matches 222; Conservative 100; Mismatches 204; Indels 60; Gaps 12;

Qy 2 DDIITATKNGKVGKGNMLTVFGGTVTAFLGIPYAOPLGRLFRKKQSLTKMSIDIMATKY 61
 Db 138 DRIVVQSSGPVGRSVTVQGREVHYTGIPIYAKPVEDIRFRKFPVAEPMHGVLDATGL 197
 Qy 62 ANSCCNIDSPFGFSGSEMMNPNTDISEDCLYINWIPAP----- 102
 Db 198 SATVOERIEYFPGFSGSEIMNPNTVSEDCLYINWIPAKKALRHGRGANGSEHPKQ 257
 Qy 103 -----KPKAT---VLIWIYGGFQGTSSLHYVDGKFLARVERIVVSMNRY 148
 Db 258 ADTDHILHNGNPQNTNGPLILWIYGGFMTSATLDIYNADIMAVGVIVIASFGYRV 317
 Qy 149 GALFLAL-PGNP---EAPNGMGLPQOOLALQWOKNIAAFGNGPKSVTLFGESAGAA 202
 Db 318 GAFGFLHLPPEMSEFAEAPGVNGLMDALAIRWIKDNNAHAFGPNEMWTLFGESAGSS 377
 Qy 203 SVSLHLSPGSHSLFTRAILQSGSFNAPMAVTSLYEARNRTLNLAKLTGCS-----REN 256
 Db 378 SVNAQLMSVTRGLVGRQMGGSTNMAPMSHMTSEAVR--IKKALINDCNAASMLKTIN 435
 Qy 257 ETEIILKLRKDDQELLINAEFVVPYPTPLSVNFGPTVVDGFLTMDLILBLGQFKTQ 316
 Db 436 PAVTMCMSVDKATISVQO--WNSYSGILSPSPAPITDGAFLPRDPMTLMTAKDXYD 493
 Qy 317 ILVGVKDEGTWFLVYG-APGFSKDNNSIITRKEFOGLKIFPPGVSEFGKESILFHYTD 375
 Db 494 ILMGNVREDEGTFLYLDYDFDKDATALPRDKYLEIMNNIIGKATQARERAIIIFQYTS 553
 Qy 376 WVDQRENYREALGVVGVNFCPALFEFTKFSSEWGNNAFFYYFHEHRSKLPWPMGM 435
 Db 554 WEGNPGYON-QQQIGRAVGVGHFTCTNEAQAALARGASVHYVYVYFTHRTSTSLMGEMG 612
 Qy 436 VMHGEIEFVFGPLERRDNYTKAEELLSRSIVKMANPAKYGNPNETONNSTSWPVFKS 495
 Db 613 VHGDEIEYFQGPLNNSLOYRVERELGKRMLSAVIEFPAKGNPAQ---DGEWENPFSK 669
 Qy 496 TEQKIYTLANTESTRIWTKLR---AQQCRFWTSFPFKVLEMTGNID 537
 Db 670 EDPVYIYFSTDK--IEKLARGPLARCSFWDYLPKRVSWAGTCD 713

A:Residues: 1-602 <GRA>
 A:Cross-references: UNIPROT:O61372; EMBL:AF025379; NID:G5091493; PIDN:AA014017.1; PID:G3
 A:Experimental source: strain N2
 C:Genetics:
 A:Gene: ace-4
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match 32.6%; Score 1012.5; DB 2; Length 602;
 Best Local Similarity 38.1%; Pred. No. 1.5e-69;
 Matches 212; Conservative 92; Mismatches 195; Indels 57; Gaps 12;

QY 4 IIAATKNGKVRGMNLTVEGTVTAFLGIPYAPQPLGRKPKQSLTKWSDIWNATKYAN 63
 DB 27 VVLETKGDKIGKTEFFFLSKKIRTFPGVPAPPAVEDFRFRKPKKQWMLYATKPYAN 86
 QY 64 SCCONIDQSPFGPFGSEKMNPTDSEDCLYLNWTPAKPKNATVLIWYGGFQGTG 123
 DB 87 ACFTDRNNTYTSFWSSEKMNANTQISBDCLYLNWTPAKPKNATVLIWYGGFQGTG 145
 QY 124 SLHAYDGKFLARVERIVSMNRYVAGLALPGNPAQNMGLFPQOLALQWVOKNIA 183
 DB 146 SLSTYDQKALSTQNVVNVNINYLGPFGFLYL-GHDPAGNMGLDQOLALHVRONTV 204
 QY 184 AFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILQSGSFNAPWATSLYEARNR 243
 DB 205 SPGNPDKAVFVGSGAGASIVAHILAPGSRGLFKNAILQSGSLENTWALNSPFAKOKS 264
 QY 244 LNLAKLTGCSRENTEIILKLRNDPOEILNENFVVPYGPPLSVNGPTV----- 294
 DB 265 EKLLELVGCKNTYVDTSMACLRIVSPQSLIS-----TNWISLYLEFPFVYVSRDKHF 319
 QY 295 -----DGFPLTMDPILLELQPKQIILVGNKDEGTWFLVYGAPG-PSKDNNS 343
 DB 320 GHLDHAHALBEGDNRD-----NLMIGMKDEGNWYNIYOLDFQDKADPP 366
 QY 344 IITRKEFGELKIFPGVSEFGESILFHYTD--WVDQREPN-YREALGVVDGYNTIC 400
 DB 367 ELNRTEFDPLDRFSIQPDILRSAAKIYSDPCKTHGKTRFRYAQGMQIVGDYFSC 426
 QY 401 PALFTYKF-----SEGNNAFFYYFEHRSKLPPEWGMGMHGEIEFVGLP 449
 DB 427 DSLMLAQFQSIIPRVKSSPQKPKGVYVYHFTOSSANPWPWKGTGMHGEIEYVGI 486
 QY 450 LERDNTKAEILSRIVKMANFAKYGNNP-ETONNSTSWPFG-KSTBEKYLTLNTES 507
 DB 487 LYSKNTKRRRQIFSRKIMQFMAFANQGPPLKRLVLSNHEPNEQNHRYRMQLRS 546
 QY 508 TRIMTKLRAQ-QCRFW 522
 DB 547 NIRPIKPKQVEQFW 562

RESULT 18
 T37255
 acetylcholinesterase (BC 3.1.1.7) 2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T37255
 R:Grau, M.; Culetto, E.; Combes, D.; Fedon, Y.; Tountant, J.P.; Arpagaus, M.
 FEBS Lett. 424, 279-284, 1998
 A:Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabditis el
 A:Reference number: Z21648; MUID:99199570; PMID:9539167
 A:Accession: T37255
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-629 <GRA>
 A:Cross-references: UNIPROT:O61371; EMBL:AF025378; NID:G5148937; PIDN:AA014016.2; PID:G5
 A:Experimental source: strain N2
 C:Genetics:
 A:Gene: ace-2
 A:Map position: 1
 C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase
 Query Match 30.5%; Score 948; DB 2; Length 629;
 Best Local Similarity 38.4%; Pred. No. 1.5e-64;
 Matches 221; Conservative 92; Mismatches 193; Indels 70; Gaps 20;

QY 3 DIIATKNGKVRGMNLTVEGTVTAFLGIPYAPQPLGRKPKQSLTKWSDIWNATKYA 62
 DB 38 DHVHTFPIGIRGVGQFPDQAKVASAFGLGVYAKPISRRFKKAEIMDRSGELEATTLA 97
 QY 63 NSCCONIDQSPFGPFGSEKMNPTDSEDCLYLNWTPAKPKNATVLIWYGGFQGTG 122
 DB 98 KCTYLTIDSAFPQPGAEEMNPPGALISBDCLYLNWTPAKPKNATVLIWYGGFQGTG 155
 QY 123 SLHAYDGKFLARVERIVSMNRYVAGLALPGNPAQNMGLFPQOLALQWVOKNIA 182
 DB 156 PSIDIVSGSFAAKEHTIVNVNINYLGPFGFLYLFGDDSPFGNMGLMDQOLALHVRONT 215
 QY 183 AAFGNPKSVTLFGESAGASVSLHLSPGSHSLFTRAILQSGSFNAPWATSLYEARNR 242
 DB 216 GAFGDSRVTFLFGESAGASVSLHLSPGSHSLFTRAILQSGSFNAPWATSLYEARNR 275
 QY 243 TNLAKLTGCSRENTEIILKLRNDPOEILNENFVVPYGPPLSVNGPTV----- 299
 DB 276 SPRLAKVNSSEPDMAIVCLRSV-PAHLVQADNITSGDIPPMTPFAVVSNDANFP 334
 QY 300 TMDPILLELG--QFKK-TQILVGNKDEGTWFLVY--GAP--GFS-----KDNNS 343
 DB 335 --QGVVQKLANQFKDVNIIIFGSYKDEBTWLPYMSLPKGFANHTISADPNRRA 392
 QY 344 IITRKEFGELKIFPGVSEFGESILFHYTD-----TDVDDQREPNYREALGVVD 395
 DB 393 LITRDHESBMAFMPYFA--GSKLVLANFMSYEHVSTNVPEER---TRDVARPLGD 447
 QY 396 YNFCPALFTYKFSR--WNNNAFFYYFEHRSKLPPEWGMGMHGEIEFVGLPERR 453
 DB 448 LFTCSLIDPADLISDIFG-NVYMYFFYRSSANPWPWKGTGMHGEIEYVGI 506
 QY 454 DNYTKA-----EILSRIVKMANFAKYGNNP-ETONNSTSWPFG-KSTBEKYLTLNTES 508
 DB 507 HLYDQTHLEBKLSLIMQIMANFANTG-----RDSWPQYNTKERAIELG-ETTL 559
 QY 509 ----RIMTKLRAOQCRFWSPFKVLEMTGNIDAE 540
 DB 560 QGKRRIISDVHGFCRW-----IDEAK 581

RESULT 19
 T27009
 hypothetical protein Y48B6A.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27009
 R:Mail, M.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20297
 A:Accession: T27009
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-584 <WIL>
 A:Cross-references: UNIPROT:Q09295; EMBL:AL110490; PIDN:CA054453.1; CESP:Y48B6A.8
 A:Experimental source: clone Y48B6A
 C:Genetics:
 A:Gene: CESP:Y48B6A.8
 A:Mutations: 24/3; 58/2; 132/2; 241/2; 461/2; 514/2
 C:Superfamily: cholinesterase; cholinesterase homology
 Query Match 30.1%; Score 937; DB 2; Length 584;
 Best Local Similarity 38.4%; Pred. No. 9.1e-64;
 Matches 208; Conservative 93; Mismatches 205; Indels 36; Gaps 16;
 6 IATKNGKVRGMNLTVEGTVTAFLGIPYAPQPLGRKPKQSLTKWSDIWNATKYANSC 65

Db 34 VQTKLGTVRGTSBDHGNKRVRSFLGVPAEPPIINHRFKKTPARPNNGTISANTLSPAC 93
QY 66 CQNIIDSPFGHSEMNPNPTDISEDCLYLNMWTPARKKNAATYLIWYGGGQOTGSSL 125
Db 94 FQGRDSYDPTFWGSEMNANTPVSEDCLYNIMAPA-DAYNLTVLWLFQGGGFWYGSPL 152
QY 126 HAYDGGKFLAVERIVVSMNRYVAGLPGFALPGNPEAPNGMGLFDQOLALQWYQKNIAP 185
Db 153 LLYDGKELATRGNTVYNINRYRPGPYLFL-DHEBDVPGNMGLDQOLALYWRDHFISF 211
QY 186 GGNPKSVTLFGESAGASVSLHLSFGSHLFTRALILOGSFNAAPAVTSLEYARRNTLN 245
Db 212 GGNPARISLVGSAGASIVAHILAPASKGLFQNGILOGSLDNKMSMDSPPRAQOKSTA 271
QY 246 LAKLTGCSRENTEIICKLNKPOEILLNBAFVVPYG---TPLSV----NFGPTVGD 297
Db 272 LADLVGNCQTKITDQACLRN-TPAQLIDINMVGNLNLEFPFAIVSKQNFPHKLDG- 329
QY 298 FLTMDPILILEGQFK-KTQILVGVNKDEGTWFLVYGAPEGSKDNNSI---ITRKEPFG 353
Db 330 -----FILRREGYSTDVNLMFGINHDGFMNIVNLAKFF-DKQSVKGLDRDBFHEC 382
QY 354 LKIFPGEVSEFGKESILFFHYTD--WVDQRPEN-YREALGVGDYNNFICPALBFTKFS 410
Db 383 VDTAFVQPELVRTAKVYVSDPKCTDPKKKTDFTYEQVQWGVGYFFCTDSIFAHNYP 442
QY 411 EW-GN--NAFFYFEHRSKLPMEWGVHGYEIEFVFGPLERRD-NYTKAEILSR 466
Db 443 KMAQNSVFFVYFDQPSANPMPKWTGVHGYEIEFVFGPLHNTTATGATKEEMDVSEK 502
QY 467 IYKMANPAKYGNPNETQ-----NSTSWPVKSTEO-KYLLTNTESTRIMTKLRAOQR 520
Db 503 VIDFWTTFANTGVPSLAKRAVGTQKIKWRYDGDHTMMNITGSEFMIOIKKVECD 562
QY 521 FW 522
Db 563 LW 564

RESULT 20
T42399
acetylcholinesterase (EC 3.1.1.7) - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42399
R/Graeb, M., Culiceto, E., Fedon, Y., Combes, D., Toutant, J.P., Arpagaus, M.
submitted to the EMBL Data Library, June 1999
A/Reference number: Z22157
A/Accession: T42399
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-607 <GRA>
A/Cross-references: UNIPROT:O61459; EMBL:AF039650; PIDN:AA014022.2
A/Map position: 2
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase

Query Match 29.9%; Score 930; DB 2; Length 607;
Best Local Similarity 38.2%; Pred. No. 3.3e-63;
Matches 207; Conservative 93; Mismatches 206; Indels 36; Gaps 16;

QY 6 IATKNGKRGKMLTYFGGTVAFLGIPYAQPPGLRFRKPKQSLTKMSDINATKYANSC 65
Db 34 VQTKLGTVRGTSBDHGNKRVRSFLGVPAEPPIINHRFKKTPARPNNGTISANTLSPAC 93
QY 66 CONIDSPFGHSEMNPNPTDISEDCLYLNMWTPARKKNAATYLIWYGGGQOTGSSL 125
Db 94 FQGRDSYDPTFWGSEMNANTPVSEDCLYNIMAPA-DAYNLTVLWLFQGGGFWYGSPL 152
QY 126 HAYDGGKFLAVERIVVSMNRYVAGLPGFALPGNPEAPNGMGLFDQOLALQWYQKNIAP 185

Db 153 LLYDGKELATRGNTVYNINRYRPGPYLFL-DOEDVPGNMGLDQOLALYWRDHFISE 211
QY 186 GGNPKSVTLFGESAGASVSLHLSFGSHLFTRALILOGSFNAAPAVTSLEYARRNTLN 245
Db 212 GGNPARISLVGSAGASIVAHILAPASKGLFQNGILOGSLDNKMSMDSPPRAQOKSTA 271
QY 246 LAKLTGCSRENTEIICKLNKPOEILLNBAFVVPYG---TPLSV----NFGPTVGD 297
Db 272 LADLVGNCQTKITDQACLRN-TPAQLIDINMVGNLNLEFPFAIVSKQNFPHKLDG- 329
QY 298 FLTMDPILILEGQFK-KTQILVGVNKDEGTWFLVYGAPEGSKDNNSI---ITRKEPFG 353
Db 330 -----FILRREGYSTDVNLMFGINHDGFMNIVNLAKFF-DKQSVKGLDRDBFHEC 382
QY 354 LKIFPGEVSEFGKESILFFHYTD--WVDQRPEN-YREALGVGDYNNFICPALBFTKFS 410
Db 383 VDTAFVQPELVRTAKVYVSDPKCTDPKKKTDFTYEQVQWGVGYFFCTDSIFAHNYP 442
QY 411 EW-GN--NAFFYFEHRSKLPMEWGVHGYEIEFVFGPLERRD-NYTKAEILSR 466
Db 443 KMAQNSVFFVYFDQPSANPMPKWTGVHGYEIEFVFGPLHNTTATGATKEEMDVSEK 502
QY 467 IYKMANPAKYGNPNETQ-----NSTSWPVKSTEO-KYLLTNTESTRIMTKLRAOQR 520
Db 503 VIDFWTTFANTGVPSLAKRAVGTQKIKWRYDGDHTMMNITGSEFMIOIKKVECD 562
QY 521 FW 522
Db 563 LW 564

RESULT 21
T33842
hypothetical protein Y44E3A.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T33842
R/Moesener, J., Graves, T., Kepler, D.
submitted to the EMBL Data Library, November 1998
A/Description: The sequence of C. elegans cosmid Y44E3A.
A/Reference number: Z21422
A/Accession: T33842
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-532 <MOE>
A/Cross-references: UNIPROT:O61371; EMBL:AF106589; PIDN:AA078228.1; GSPDB:GN00019; CESP:1
A/Experimental source: strain Bristol N2; clone Y44E3A
C/Keywords: CESP:Y44E3A.2
A/Map position: 1
A/Intons: 16/3; 84/3; 143/2; 219/3; 298/3; 440/2
C/Superfamily: cholinesterase; cholinesterase homology

Query Match 28.7%; Score 893; DB 2; Length 532;
Best Local Similarity 40.8%; Pred. No. 1.9e-60;
Matches 201; Conservative 79; Mismatches 169; Indels 44; Gaps 16;

QY 19 TFGGTVAFLGIPYAQPPGLRFRKPKQSLTKMSDINATKYANSCQNIIDSPFGFG 78
Db 17 TFGGAKYSAPLGVYAKPPIGSRFRKMAEMIDMSGELEAKTKCYLITDIAFPQFG 76
QY 79 SEMNPNPTDISEDCLYLNMWTPARKKNAATYLIWYGGGQOTGSSLHAYDGGKFLAVER 138
Db 77 AEMNPNPGALISEDCLMNNTIV--PEHDGDSVMMWYIYGGSFSGTSLDYSGVFAKEH 134
QY 139 VIVSMNRYVAGLPGFALPGNPEAPNGMGLFDQOLALQWYQKNIAPFGNPKSVTLFGES 198
Db 135 TIVNVMYVRIGPGLFYGDSPIQGNMGLMDQOLALRWHEHNIQAFGGDRSVTLFGES 194
QY 199 AGAASVSLHLSFGSHLFTRALILOGSFNAAPAVTSLEYARRNTLNLAKTGCSRENTE 258
Db 195 AGSASTTAHLFAPNSHKYFNNTIAKSGSTINSWASATPPTMLDLSRLAKKNCSSPDM 254

QY 259 EIIKCLNKKPOEILLNEAFV--PYGTPLSVNFGP-TVDGDLTDMEDLLELG-QFK 313
 Db 255 AIVKCLASV-PAHVQAEADNIGSDIGPMTFAVVPVSDANF--QGDVQKLANQKFK 311
 QY 314 K-TQILVGVNDEGTWLVY--GAP--GFS-----KNNSTIRKEQEGKTFP 359
 Db 312 KDVAIIIGSVNDEGTWLVY--GAP--GFS-----KNNSTIRKEQEGKTFP 371
 QY 360 GVSEFGKESILFHY-----TDMVDQDQRPENYREALGVGDPNFCIPALFTKKESE 411
 Db 372 YFA--GSKLVANAMNSYEHSTSNVPER--YRDGARFLGDLFFTCISLIDPADLISD 426
 QY 412 --WGNNAFFYYFEHRSKLPWPMWGVNHYEIEFFVGLPERDNTYKA---EELISR 465
 Db 427 NIFG-NVNYMYFTYRSSANPMWKMVGVMHGYEIVAFQPYWRPHLYQDTLDEKRLSS 485
 QY 466 SIYKMANPFAKY 478
 Db 486 IIMQIMANFANTG 498

RESULT 22

A34329
 60K esterase (EC 3.1.1.-) isoform 2 - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
 C/Accession: A34329
 R/Octols: J.
 J. Biol. Chem. 264, 12533-12545, 1989
 A/Title: Isolation, properties, and the complete amino acid sequence of a second form of
 A/Reference number: A34329; PMID:89308686; PMID:2745458
 A/Accession: A34329
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-532 <OZO>
 C/Cross-references: UNIPROT:P14943
 C/Superfamily: cholinesterase; cholinesterase homology
 C/Keywords: carboxylic ester hydrolase
 F/32-517/Domain: cholinesterase homology <CH>
 F/201,430/Active site: Ser, His #status predicted

Query Match 24.2%; Score 754; DB 2; Length 532;
 Best Local Similarity 36.1%; Pred. No. 8.5e-50;
 Matches 199; Conservative 90; Mismatches 202; Indels 60; Gaps 22;

QY 8 TKNGKXKGMULTVFG--GTYAFEGIPYAPQPLGRLEPKKQSLTKXSDINNAKTVNSC 65
 Db 10 THTGQVRGSLVHVEGTDAVHTFLGIPAKPLGLRPAPEPAEAMSGVADGTSLPAMC 69
 QY 66 CONT---DQSPFGHSEMMNPTDLSBDCLYLVWVLP--APKPKNATVLIWYGGGFOT 120
 Db 70 LQNLAIMDQVLLHFP--PSIPMSBDCLYLVWVLP--APKPKNATVLIWYGGGFOT 126
 QY 121 GTSSLHAYDGFELARVERVIVSNMYRGALGFALPGNPEAPNGMLFDQQLALQWVQK 180
 Db 127 GMSM--YDGSALAFEDVVVVTIQRVLGVLFPS--TGDDAATGNHGYLDQVALRWQK 183
 QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSGSHSLFTRALQSGSFAAPAVALSYEAR 240
 Db 184 NIAAFGNPKSVTLFGESAGAGTSVSHVSLFPGALMESIVALLPGLITSSSEV 243
 QY 241 NRTNLAKLNGCSSENEETIKKLRNKDPOIL-LINEAFVVPYGPPLSVNNGPVPVDDGFL 299
 Db 244 STV--VANLSRCGVADSETLVRCRAKSEEMLITVFMILPG-----VVDGYFL 292
 QY 300 TDMEDLLELGQFKKTOILVGVNDEGTW---FLVYGAPGFSKDNNSIIRKEFOBGLK 355
 Db 293 PRHREELALADFPVPSITGINNDEGWIIPKLLAIDPBERDRQAM--RLIMHQATK 350
 QY 356 --TFPGVSEKGSILFHTYDWDQDQRPENYREALGVGDPNFCIPALFTKKESE 413
 Db 351 QLMPLPALGDL---LMDYVGSNED--PKILMAQFQEMADAMFVMPALR-VAHLQRSH 403

QY 414 NNAFFYYFEHRS--KLPMWPMWGVNHYEIEFFVGLPERDNTYKA---EELISR 464
 Db 404 APYFYEFQRPSPFTKOLRPPHVRADHGVFVFRSHLFGSKVPL-----TEEBELLS 457
 QY 465 RSIYKMANPFAKGNPNETQNNSTWPFVFKSTOCKYTLTNESTRITKLRACQCRWTS 524
 Db 458 RRVKRYANPARNNPN--GEGLAHPLF-DLDQRYQLNMQPA-VQALKARRLOFWTH 513
 QY 525 FFP-KVLEMTG 534
 Db 514 TLPRVQVELNG 524

RESULT 23

G39768
 cholinesterase (EC 3.1.1.8) - rhesus macaque (fragment)
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
 C/Accession: G39768
 R/Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogi
 J. Biol. Chem. 266, 6966-6974, 1991
 A/Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase
 A/Reference number: A39768; PMID:91201346; PMID:2016308
 A/Accession: G39768
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-141 <ARP>
 A/Cross-references: UNIPROT:P32751; GB:M62777; NID:g342078; PIDN:AAA36836.1; PID:g342079
 C/Superfamily: cholinesterase; cholinesterase homology
 C/Keywords: carboxylic ester hydrolase; glycoprotein
 F/1-141/Domain: cholinesterase homology (fragment) <CH>

Query Match 24.2%; Score 753; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 NIDQSPFGHSEMMNPTDLSBDCLYLVWVLP--APKPKNATVLIWYGGGFOTGSSLHY 127
 Db 1 NIDQSPFGHSEMMNPTDLSBDCLYLVWVLP--APKPKNATVLIWYGGGFOTGSSLHY 60
 QY 128 YDGFELARVERVIVSNMYRGALGFALPGNPEAPNGMLFDQQLALQWVQKIAFP 187
 Db 61 YDGFELARVERVIVSNMYRGALGFALPGNPEAPNGMLFDQQLALQWVQKIAFP 120
 QY 188 NPKSVTLFGESAGAASVSLH 208
 Db 121 NPKSVTLFGESAGAASVSLH 141

RESULT 24

A57701
 sterol esterase (EC 3.1.1.13) precursor - mouse
 N/Alternate names: bile salt-stimulated lipase; carboxyl ester lipase; cholesterol esterase
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C/Accession: A57701; J04384
 R/Lidmer, A.S.; Kamius, M.; Lundberg, L.; Bjursell, G.; Nilsson, J.
 Genomics 29, 115-122, 1995
 A/Title: Molecular cloning and characterization of the mouse carboxyl ester lipase gene
 A/Reference number: A57701; PMID:96079098; PMID:8530060
 A/Accession: A57701
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-599 <LID>
 A/Cross-references: UNIPROT:Q64285; GB:U37386; NID:g1049321; PIDN:AA52279.1; PID:g1049321
 R/Mackay, K.; Lam, R.M.
 Gene 165, 255-259, 1995
 A/Title: Characterization of the mouse pancreatic/mammary gland cholesterol esterase-enc
 A/Reference number: J04384; PMID:96096531; PMID:8522186
 A/Accession: J04384
 A/Molecule type: mRNA
 A/Residues: 1-599 <MAC>
 A/Cross-references: GB:U33169; NID:g1046362; PIDN:AAA92088.1; PID:g1046363

A:Experimental source: mammary gland
 C:Comment: This enzyme is synthesized in the pancreas and is transported to the intestine
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; cholinesterase; heparin binding; mammary gland; par
 C:KeyWords: carboxylic ester hydrolase; cholinesterase; heparin binding; mammary gland; par
 F/1-20/Domains: signal sequence #status predicted <SIG>
 F/21-599/Product: steric esterase #status predicted <MAT>
 F/51-585/Domains: cholinesterase homology <CH>
 F/81-86/Region: heparin binding #status predicted
 F/214,340,455/Active site: Ser, Asp, His #status predicted

C:Genetics:

A:Gene: Case

C:Superfamily: cholinesterase; cholinesterase homology

C:KeyWords: carboxylic ester hydrolase; cholinesterase; heparin binding; mammary gland; par

F/1-20/Domains: signal sequence #status predicted <SIG>

F/21-599/Product: steric esterase #status predicted <MAT>

F/51-585/Domains: cholinesterase homology <CH>

F/81-86/Region: heparin binding #status predicted

F/214,340,455/Active site: Ser, Asp, His #status predicted

Query Match 23.5%; Score 732; DB 2; Length 599;

Best Local Similarity 33.0%; Pred. No. 4,9e-48;

Matches 189; Conservative 91; Mismatches 212; Indels 80; Gaps 22;

6 IATNGKVRGMN--LTVPGG-TYTAFLGIPYAPQPLRLAFKKPQSLTKMSDIMNATKXA 62

26 VYTEGVEGVNKKLSLGGDSVDIFKGIIPAAK--TLENPRHPCOGTLKATNFK 81

63 NSCCNIDSPFGHSEMMNPTDLSBDCIYLNWIPAPKPK--NATVLIWYGGPQT 119

82 KRCIQ-----ATITQDNTYGGEDCLYINWIPQGRKQSHLPMWMIYGGAF 130

120 TGTG-----SLHYDGKFLANVERVYVSNRYGALGFLALPQNPAPGMMGLPDQOL 173

131 MGSGGANFLKRYLYDGEIATRGAVIVTFNRYVGPGLFS--TGDNLPGNFGRLDQHM 189

174 ALQWOKNIAAFGNGPKSVTLFGESAGASVSLHLSPGSHSLFTRAILQSGSFNAPAV 233

190 ALAWKNTIAPGDDPNITTFGSGAGASVSLQTLSPYNGKILRAISQSGMALSPWAI 249

224 --TSLYARNRTMLAKLTGCSRENETEIIKCLRNKPOEILNEAFVVP-----YETPL 286

250 QKNPLFWAK---TIAKKVGCPTEDTGMAACLITPRAALT--AYKLPLKCKOGEYVVA 303

287 SVNRPPTVDGFLTPMDPILLEGQPKT---QILVGNKDEGTWPLVYGAPGSKDNNS 343

304 YLAFPLVIDGFLTPDDP-----INLYNTADIDYAGINMNGHLFATIDVPAVDKQOT 358

344 IITRKEF-----QELKIFPPGVSEFGKESILFHYTD--WVDDQRPENYREALGDV 393

359 -VTEDPFLRYSGHVYAKGK-----GAQATFDIYTESMAQDPQEMKKTIVVAFE 408

394 GDYNICP---ALFTFKKFESEWGNNAFYFEEHRSKLPMBEMGVMHGIEFVGLPL 450

409 TDVLFILPTEIALAQHKAAK-SAKTYGILFSPHPRMPTIPKMGADHADLDLYVFGKPF 467

451 ERDNYTKAEELISRSIVKMANFAKYNPNETQNN--TSMVPEKSTEOKYLTILNES 507

468 ATPIGRPODRAVSRAKMIATWTFNPARSGDPN--MANSVPVTHWYTYLLENQNYLDTITKI 525

508 TRIMTK--LRAQOCRFMTSPFPKVLMTGNID 537

526 TSASMKHEHREKFLKFWATFEVLPVTGDD 557

RESULT 25

A33668

sterol esterase (EC 3.1.1.13) precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33668

R:Kyte, E.M.; Wiegand, R.C.; Lange, L.G.

Biochem. Biophys. Res. Commun. 164, 1302-1309, 1989

A:Title: Cloning of the bovine pancreatic cholesterol esterase/lysophospholipase.

A:Reference number: A33668; PMID:90073663; PMID:2590203

A:Accession: A33668

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-597 <KYG>

A:Cross-references: UNIPROT:P30122; GB:M28402; NID:G598081; PIDN:AAA56788.1; PID:G598082
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 C:KeyWords: carboxylic ester hydrolase
 F/48-583/Domains: cholinesterase homology <CH>

Query Match 23.4%; Score 729; DB 2; Length 597;

Best Local Similarity 32.0%; Pred. No. 8.3e-48;

Matches 181; Conservative 98; Mismatches 212; Indels 74; Gaps 19;

6 IATNGKVRGMN--LTVPGG-TYTAFLGIPYAPQPLRLAFKKPQSLTKMSDIMNATKXA 63

24 VYTEGVEGVNKKLSLGGDSVDIFKGIIPAAK--LEKPRHPCOGTLKAKSFKK 80

64 SCCCNIDSPFGHSEMMNPTDLSBDCIYLNWIPAPKPK--NATVLIWYGGPQT 120

81 KRCIQ-----ATITQDNTYGGEDCLYINWIPQGRKQSHLPMWMIYGGAF 129

121 GTS-----SLHYDGKFLANVERVYVSNRYGALGFLALPQNPAPGMMGLPDQOL 174

130 GASQGANFLKRYLYDGEIATRGAVIVTFNRYVGPGLFS--TGDNLPGNFGRLDQHM 188

175 ALQWOKNIAAFGNGPKSVTLFGESAGASVSLHLSPGSHSLFTRAILQSGSFNAPAV 234

189 IAWKNTIAPGDDPNITTFGSGAGASVSLQTLSPYNGKILRAISQSGMALSPWAI 248

235 S--TSLYARNRTMLAKLTGCSRENETEIIKCLRNKPOEILNEAFVVPYETP-----LS 287

249 QDPLFWAK---RIAEKVGCPVDTSKMAAGCLIKITPRAALT--AYKLPLDSTEVPKLHY 302

288 VNFPGVPODPLTPMDPILLEGQPKTQILVGNKDEGTWPLVYGAPGSKDNNSITR 347

303 LSFVPLVIDGFLTPDDVNL--YANAADVDYIAGTNDMNGHLFVGNVDVPAIN--SNKQDYTE 359

348 KEF-----QELKIFPPGVSEFGKESILFHYTD--WVDDQRPENYREALGDV 397

360 EDDYKVLGSLVYTKGR-----GANATVEYVTEPMAQSSQETKKTWVDELTEPIL 410

398 FICPALEFK-----KSEWGNNAFYFEEHRSKLPMBEMGVMHGIEFVGLPLE 451

411 FLIP-----TKIYVAOHKSHAKSANTYTYLFSQPSRMPTIPKMGADHADLDLYVFGKPPA 466

452 RRDNYTKAEELISRSIVKMANFAKYNPNETQNN--TSMVPEKSTEOKYLTILNES 508

467 TPLGYPADRTYSKAMIAWTFNPARSGDPN--MANSVPVTHWYTYLLENQNYLDTITKI 526

509 RIMTKLRAQOCRFMTSPFPKVLMT 533

527 SMKLHLRTWYLPQWLTQALPTV 551

Search completed: January 6, 2005, 10:00:29

Job time: 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 09:41:48 ; Search time 160 Seconds
(without alignments)
1286.941 Million cell updates/sec

Title: US-09-748-739a-2_COPY_29_602
Perfect score: 3110
Sequence: 1 EDIIIIATKNGKVRGNMLTV.....MDWKQFNFDYTSKSCVGL 574

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3110	100.0	574	7 ABW00722	ABW00722 Human but
2	3110	100.0	602	5 AAO18897	AAO18897 Human but
3	3107	99.9	574	8 ADR01039	ADR01039 Human but
4	3103	99.8	574	8 ADR01047	ADR01047 Human but
5	3102	99.7	574	8 ADR01051	ADR01051 Human but
6	3102	99.7	574	8 ADR01035	ADR01035 Human but
7	3101	99.7	574	8 ADR01041	ADR01041 Human but
8	3100	99.7	574	8 ADR01037	ADR01037 Human but
9	3099	99.6	574	5 AAO18944	AAO18944 Human but
10	3098	99.6	574	8 ADR01049	ADR01049 Human but
11	3096	99.5	574	5 AAE25235	AAE25235 Human but
12	3096	99.5	574	5 AAO18982	AAO18982 Human but
13	3096	99.5	574	5 AAO18988	AAO18988 Human but
14	3096	99.5	574	6 ABR62391	ABR62391 Human but
15	3096	99.5	574	7 ABW00695	ABW00695 Human but
16	3096	99.5	574	8 ADP44639	ADP44639 Human but
17	3096	99.5	574	8 ADR01077	ADR01077 Human but
18	3096	99.5	602	3 AAY59235	AAY59235 Human but
19	3096	99.5	602	3 AAY49471	AAY49471 Human but
20	3096	99.5	602	3 AAY44573	AAY44573 Human but
21	3096	99.5	602	6 ABR62392	ABR62392 Human but
22	3096	99.5	602	7 ADR90908	ADR90908 Human but
23	3095	99.5	574	8 ADR01045	ADR01045 Human but
24	3093	99.5	574	8 ADR01059	ADR01059 Human but
25	3093	99.5	574	8 ADR01075	ADR01075 Human but

26	3092	99.4	574	5 AAO18977	AAO18977 Human but
27	3092	99.4	574	7 ABW00723	ABW00723 Human but
28	3092	99.4	574	8 ADR01080	ADR01080 Human but
29	3092	99.4	602	3 AAY44574	AAY44574 Human but
30	3091	99.4	574	5 AAO18979	AAO18979 Human but
31	3091	99.4	574	5 AAO18980	AAO18980 Human but
32	3091	99.4	602	3 AAY49483	AAY49483 Human but
33	3090	99.4	574	5 AAO18945	AAO18945 Human but
34	3090	99.4	574	5 AAO18945	AAO18945 Human but
35	3090	99.4	574	8 ADP44833	ADP44833 Human but
36	3090	99.4	574	8 ADR01073	ADR01073 Human but
37	3090	99.4	602	2 AAR37442	AAR37442 Full-length
38	3089	99.3	574	5 AAO18981	AAO18981 Human but
39	3089	99.3	574	5 AAO18940	AAO18940 Human but
40	3089	99.3	574	8 ADR01079	ADR01079 Human but
41	3089	99.3	574	8 ADR01078	ADR01078 Human but
42	3089	99.3	602	3 AAY49474	AAY49474 Human but
43	3089	99.3	602	3 AAY49475	AAY49475 Human but
44	3089	99.3	602	3 AAY49475	AAY49475 Human but
45	3088	99.3	574	7 ABW00724	ABW00724 Human but
46	3088	99.3	574	8 ABW00725	ABW00725 Human but
47	3088	99.3	574	8 ADP44738	ADP44738 Human but
48	3088	99.3	574	8 ADR01055	ADR01055 Human but
49	3088	99.3	574	8 ADR01061	ADR01061 Human but
50	3088	99.3	574	8 ADR01065	ADR01065 Human but
51	3088	99.3	574	8 ADR01071	ADR01071 Human but
52	3088	99.3	574	8 ADR01069	ADR01069 Human but
53	3088	99.3	602	3 AAY49472	AAY49472 Human but
54	3087	99.3	602	3 AAY49476	AAY49476 Human but
55	3087	99.3	574	5 AAO18978	AAO18978 Human but
56	3087	99.3	574	8 ADR01063	ADR01063 Human but
57	3087	99.3	574	8 ADR01043	ADR01043 Human but
58	3087	99.3	602	3 AAY49477	AAY49477 Human but
59	3086	99.2	574	5 AAO18942	AAO18942 Human but
60	3086	99.2	574	5 AAO18941	AAO18941 Human but
61	3086	99.2	574	8 ADP44765	ADP44765 Human but
62	3086	99.2	574	8 ADP44821	ADP44821 Human but
63	3086	99.2	574	8 ADR01057	ADR01057 Human but
64	3086	99.2	574	8 ADR01067	ADR01067 Human but
65	3085	99.2	574	5 AAO18899	AAO18899 Human but
66	3085	99.2	574	5 AAO18943	AAO18943 Human but
67	3085	99.2	574	5 AAO18901	AAO18901 Human but
68	3085	99.2	574	5 AAO18902	AAO18902 Human but
69	3085	99.2	574	8 ADP44800	ADP44800 Human but
70	3085	99.2	574	8 ADP44771	ADP44771 Human but
71	3085	99.2	602	3 AAY49484	AAY49484 Human but
72	3085	99.2	602	3 AAY49478	AAY49478 Human but
73	3084	99.2	574	5 AAO18976	AAO18976 Human but
74	3084	99.2	574	8 ADP44776	ADP44776 Human but
75	3084	99.2	574	8 ADP44810	ADP44810 Human but
76	3084	99.2	574	8 ADP44758	ADP44758 Human but
77	3084	99.2	574	8 ADP44780	ADP44780 Human but
78	3084	99.2	574	8 ADP44806	ADP44806 Human but
79	3084	99.2	574	8 ADR01053	ADR01053 Human but
80	3084	99.2	602	3 AAY49486	AAY49486 Human but
81	3084	99.2	602	3 AAY49485	AAY49485 Human but
82	3084	99.2	602	3 AAY49488	AAY49488 Human but
83	3083	99.1	574	8 ADP44762	ADP44762 Human but
84	3083	99.1	574	8 ADP44769	ADP44769 Human but
85	3083	99.1	574	8 ADP44812	ADP44812 Human but
86	3083	99.1	574	8 ADP44770	ADP44770 Human but
87	3083	99.1	574	8 ADP44755	ADP44755 Human but
88	3083	99.1	574	8 ADP44772	ADP44772 Human but
89	3083	99.1	574	8 ADP44797	ADP44797 Human but
90	3083	99.1	574	8 ADP44739	ADP44739 Human but
91	3083	99.1	574	8 ADP44744	ADP44744 Human but
92	3083	99.1	602	3 AAY49487	AAY49487 Human but
93	3083	99.1	602	3 AAY49487	AAY49487 Human but
94	3082	99.1	574	5 AAO18960	AAO18960 Human but
95	3082	99.1	574	5 AAO18971	AAO18971 Human but
96	3082	99.1	574	5 AAO18933	AAO18933 Human but
97	3082	99.1	574	5 AAO18935	AAO18935 Human but
98	3082	99.1	574	8 ADP44756	ADP44756 Human but

99 3082 99.1 574 8 ADP44757
100 3082 99.1 574 8 ADP44764

ADP44757 Human but
ADP44764 Human but

ALIGNMENTS

RESULT 1

ABM00722 standard; protein; 574 AA.

ABM00722;

15-JAN-2004 (first entry)

Human butyrylcholinesterase variant protein (A328W).

Human; butyrylcholinesterase; enzyme; mutant; mutein; variant.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 328 /note= "Wild-type Ala substituted with Trp"

XX US2003096401-A1.

XX 22-MAY-2003.

XX 28-NOV-2001; 2001US-00997209.

XX 28-NOV-2000; 2000US-0367370P.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI; 2003-786991/74.

XX Cell composition comprises non-yeast eukaryotic cells having diverse
XX population of variant nucleic acids or heterologous nucleic acid
XX fragments, useful for identifying polypeptide with optimized activity.

XX Example 11; Page; 0pp; English.

XX The invention relates to a cell composition comprising a population of
XX non-yeast eukaryotic cells containing diverse population of variant
XX nucleic acids, or heterologous nucleic acid fragments with distinct
XX species of nucleic acid fragments, where each of the variant nucleic
XX acids or heterologous nucleic acid fragments are expressed in different
XX cell and located within each cell at an identical site in the genome. The
XX invention is useful for identifying polypeptide with optimised activity
XX and for identifying a polypeptide receptor for a ligand. The present
XX sequence is human butyrylcholinesterase variant protein. This sequence is
XX used in the exemplification of the invention. Note: This sequence is not
XX shown in the specification but is derived from the human
XX butyrylcholinesterase wild-type protein (ABM00695) shown in figure 8 of
XX the specification

XX Sequence 574 AA;

Query Match 100.0%; Score 3110; DB 7; Length 574;

Best Local Similarity 100.0%; Pred. No. 2.2e-278; Indels 0; Gaps 0;

Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVGKNTLVFGITVTAFLGIPYAOPPIGLRFRKKPQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVGKNTLVFGITVTAFLGIPYAOPPIGLRFRKKPQSLTKWSDIWNATK 60
QY 61 YANSCCONIDQSPFGHSEMMNPNTDSEDCLYLNWVTPAKPKNAATLWYGGGQPT 120
DB 61 YANSCCONIDQSPFGHSEMMNPNTDSEDCLYLNWVTPAKPKNAATLWYGGGQPT 120

QY 121 GTSSLHYVDGKFLAVERVIIVSNMYRYGALGFALPQNPAPGNGLFDQQLAQWQK 180
DB 121 GTSSLHYVDGKFLAVERVIIVSNMYRYGALGFALPQNPAPGNGLFDQQLAQWQK 180
QY 181 NIAAFGPNKSVTLFGESAGAAVSGLHLSRQSHSLFTRAILQSGSFNAPNAVTSYEAR 240
DB 181 NIAAFGPNKSVTLFGESAGAAVSGLHLSRQSHSLFTRAILQSGSFNAPNAVTSYEAR 240
QY 241 NRTLNIAKLTCGSRNEMTEIICLNKPOEILNEAFVPGTPLSYNFGPTVDGDEL 300
DB 241 NRTLNIAKLTCGSRNEMTEIICLNKPOEILNEAFVPGTPLSYNFGPTVDGDEL 300
QY 301 DMPDILIEIGQFKQTQILVGNKDEGTWFLYVAGPFSKDNNSITTRKEFOGLKIFPPG 360
DB 301 DMPDILIEIGQFKQTQILVGNKDEGTWFLYVAGPFSKDNNSITTRKEFOGLKIFPPG 360
QY 361 VSEFGKESILFHYTWDQRPENYREALGVYGVNFIQPLAETFKKPESEGNNAFFY 420
DB 361 VSEFGKESILFHYTWDQRPENYREALGVYGVNFIQPLAETFKKPESEGNNAFFY 420
QY 421 FEHRSKLPMPPEMGVHGIEIEFVGLPLEBRDNTYKAEBILSRSIYKMANPAKYGNP 480
DB 421 FEHRSKLPMPPEMGVHGIEIEFVGLPLEBRDNTYKAEBILSRSIYKMANPAKYGNP 480
QY 481 NETQNNSTWPFYFKSTQKYTLTNTSTRIMTKLPAQOCRFMTSPFKYLEMTGNIDEAE 540
DB 481 NETQNNSTWPFYFKSTQKYTLTNTSTRIMTKLPAQOCRFMTSPFKYLEMTGNIDEAE 540
QY 541 MEWKAGFHRMNNYMDMKNOFNDYTSKESCVGL 574
DB 541 MEWKAGFHRMNNYMDMKNOFNDYTSKESCVGL 574

RESULT 2

AAO18897 standard; protein; 602 AA.

AAO18897;

02-DEC-2002 (first entry)

Human butyrylcholinesterase variant #1.

Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;

cocaine addition; antiaddictive; antidote.

XX Homo sapiens.

XX WO200264796-A2.

XX 22-AUG-2002.

XX 21-DEC-2001; 2001WO-US050450.

XX 26-DEC-2000; 2000US-00748739.

XX 20-DEC-2001; 2001US-00032233.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.

XX (UTNE-) UNIV NEBRASKA MEDICAL CENT.

XX Lockridge O, Watkins JD, Pancook JD;

XX WPI; 2002-636633/68.

XX N-PSDB; AAL49276.

XX New human butyrylcholinesterase variant polypeptides, useful for treating

XX cocaine-induced conditions.

XX Claim 1; Fig 1; 150pp; English.

XX The present invention relates to mutants of human butyrylcholinesterase.

XX The enzymes have an increased cocaine hydrolysis activity and can be used

CC for treating a cocaine-induced condition. The present sequence is a
 CC protein shown in the exemplification of the invention

XX Sequence 602 AA;

Query Match 100.0%; Score 3110; DB 5; Length 602;
 Best Local Similarity 100.0%; Pred. No. 2,4e-278;
 Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKRGKGMVLTVFGGTVTAFLGIPYAQPLGLRFRKPKQSLTKMSDIMNATK 60
 DB 29 EDDIIATKNGKRGKGMVLTVFGGTVTAFLGIPYAQPLGLRFRKPKQSLTKMSDIMNATK 88
 QY 61 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYINWIPAPKPKATVLIWYGGGFQ 120
 DB 89 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYINWIPAPKPKATVLIWYGGGFQ 146
 QY 121 GTSSLHYDGKFLARVERVIVSMNRYVAGLGFALPGNBPAGNMGFLPQOALALQWVOK 180
 DB 149 GTSSLHYDGKFLARVERVIVSMNRYVAGLGFALPGNBPAGNMGFLPQOALALQWVOK 208
 QY 181 NIAFGGNPKSVTLFGSAGAAVSJLHLSPGSHSLFTRAILQSGSFNAAPAVTSLYEAR 240
 DB 209 NIAFGGNPKSVTLFGSAGAAVSJLHLSPGSHSLFTRAILQSGSFNAAPAVTSLYEAR 268
 QY 241 NRTLNIAKLTCGSRNTEIILKLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 300
 DB 269 NRTLNIAKLTCGSRNTEIILKLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 328
 QY 301 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360
 DB 329 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 388
 QY 361 VSEFGKESILFHTDWDQDPPENYRREALDVGVDYVFCIPALEFTKCFSEMGNAFFY 420
 DB 389 VSEFGKESILFHTDWDQDPPENYRREALDVGVDYVFCIPALEFTKCFSEMGNAFFY 448
 QY 421 FEHRSSKLPPEWNGVGHGEIEFVFGPLPERDNTTKAEIISRSIVKMANPAKXGNP 480
 DB 449 FEHRSSKLPPEWNGVGHGEIEFVFGPLPERDNTTKAEIISRSIVKMANPAKXGNP 508
 QY 481 NETONNSTSWPVFKSTQKTLTNTBSTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 540
 DB 509 NETONNSTSWPVFKSTQKTLTNTBSTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 568
 QY 541 WEWKAGFHRNNYMMDKQNFNDYTSKESCVGL 574
 DB 569 WEWKAGFHRNNYMMDKQNFNDYTSKESCVGL 602

RESULT 3

ID ADR01039 standard; protein; 574 AA.

AC ADR01039;

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A328W/V331L variant.

XX butyrylcholinesterase; cocaine-induced condition;

KM cocaine-based butyrylcholinesterase substrate; cocaine-overdose;

XX cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.

PN US2004121970-A1.

PF 20-DEC-2002; 2002US-00324466.

XX

PR 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.

PA (PANCO/) PANCOOK J D.

XX WATKINS JD, Pancook JD;

XX WPI; 2004-468195/44.

DR N-PSDB; ADR01038.

XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine

PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

PS Claim 1; SEQ ID NO 6; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)

CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID

CC NOS: 2-42) or their functional fragments. Also described are: a nucleic

CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416

CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a

CC cocaine-induced condition; and a method of hydrolyzing a cocaine-based

CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant

CC polypeptide comprising any of the 21 sequences of 57 amino acids each

CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the

CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The

CC butyrylcholinesterase variant polypeptides and nucleic acids and methods

CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or

CC cocaine addiction. This is the amino acid sequence of a human

CC butyrylcholinesterase variant.

XX Sequence 574 AA;

QY 1 EDDIIATKNGKRGKGMVLTVFGGTVTAFLGIPYAQPLGLRFRKPKQSLTKMSDIMNATK 60

DB 1 EDDIIATKNGKRGKGMVLTVFGGTVTAFLGIPYAQPLGLRFRKPKQSLTKMSDIMNATK 60

QY 61 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYINWIPAPKPKATVLIWYGGGFQ 120

DB 61 YANSCCNIDQSPFGHSGEMNPNPTDLSBDCLYINWIPAPKPKATVLIWYGGGFQ 120

QY 121 GTSSLHYDGKFLARVERVIVSMNRYVAGLGFALPGNBPAGNMGFLPQOALALQWVOK 180

DB 121 GTSSLHYDGKFLARVERVIVSMNRYVAGLGFALPGNBPAGNMGFLPQOALALQWVOK 180

QY 181 NIAFGGNPKSVTLFGSAGAAVSJLHLSPGSHSLFTRAILQSGSFNAAPAVTSLYEAR 240

DB 181 NIAFGGNPKSVTLFGSAGAAVSJLHLSPGSHSLFTRAILQSGSFNAAPAVTSLYEAR 240

QY 241 NRTLNIAKLTCGSRNTEIILKLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 300

DB 241 NRTLNIAKLTCGSRNTEIILKLRNDPOEILINAEFVVPYGTPLSVNFGPTVDGDFLT 300

QY 301 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360

DB 301 DMPDIIILEGQPKKTQILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHTDWDQDPPENYRREALDVGVDYVFCIPALEFTKCFSEMGNAFFY 420

DB 361 VSEFGKESILFHTDWDQDPPENYRREALDVGVDYVFCIPALEFTKCFSEMGNAFFY 420

QY 421 FEHRSSKLPPEWNGVGHGEIEFVFGPLPERDNTTKAEIISRSIVKMANPAKXGNP 480

DB 421 FEHRSSKLPPEWNGVGHGEIEFVFGPLPERDNTTKAEIISRSIVKMANPAKXGNP 480

QY 481 NETONNSTSWPVFKSTQKTLTNTBSTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 540

DB 481 NETONNSTSWPVFKSTQKTLTNTBSTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDEAE 540

QY 541 WEWKAGFHRNNYMMDKQNFNDYTSKESCVGL 574

DB 541 WEWKAGFHRNNYMMDKQNFNDYTSKESCVGL 574

DB 541 MEWKAGFHRMNNYMDWKQFNDYTSKESCVGL 574

RESULT 4
ADRO1047
ID ADRO1047 standard; protein; 574 AA.
XX
AC ADRO1047;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/S287G/A199S variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOCK J D.
XX
PI Wackins JD, Pancook JD;
XX
XX WPI; 2004-468195/44.
DR N-PSDB; ADRO1046.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
-induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
PS Claim 1; SEQ ID NO 14; 131pp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
NOS: 2-42) or their functional fragments. Also described are: a nucleic
acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
cocaine-induced condition; and a method of hydrolysing a cocaine-based
butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
polypeptide comprising any of the 21 sequences of 57 amino acids each
(EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
butyrylcholinesterase variant polypeptides and nucleic acids and methods
are useful in treating cocaine-induced condition i.e. cocaine-overdose or
cocaine addiction. This is the amino acid sequence of a human
butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match 99.8%; Score 3103; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 9.9e-278;
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIITATNGKVGKAMNLTIVGGYTAFLGIPYAPPIGRIRFKKPSQSLTWSIMATK 60
DB 1 EDDIIITATNGKVGKAMNLTIVGGYTAFLGIPYAPPIGRIRFKKPSQSLTWSIMATK 60
QY 61 YANSCCQNDISFPGFSGEMMNPTDISEDCLYANWIPAPKPKNAATVLIIWYGGGQOT 120
DB 61 YANSCCQNDISFPGFSGEMMNPTDISEDCLYANWIPAPKPKNAATVLIIWYGGGQOT 120
QY 121 GTSSLIHVVDGKFLARVERIVVSMNYRGALGFLALPQNPAFGNMGFLDQOLALQWYOK 180
DB 121 GTSSLIHVVDGKFLARVERIVVSMNYRGALGFLALPQNPAFGNMGFLDQOLALQWYOK 180

DB 121 GTSSLIHVVDGKFLARVERIVVSMNYRGALGFLALPQNPAFGNMGFLDQOLALQWYOK 180
QY 181 NTAAREGNPKSVTLRGESAGASVSLHLSPGSHLFTFRAIIQSGSPNAPMAVTSLYEAR 240
DB 181 NTAAREGNPKSVTLRGESAGASVSLHLSPGSHLFTFRAIIQSGSPNAPMAVTSLYEAR 240
QY 241 NRTLANLAKLTGCSRENETEIIKCLRNKDPQELILNEAFVVPYGTPLSVNFGPTVDGFLT 300
DB 241 NRTLANLAKLTGCSRENETEIIKCLRNKDPQELILNEAFVVPYGTPLSVNFGPTVDGFLT 300
QY 301 DMPDILILEIGQFKQTQIIVGVNKDEGTWFLVYGAPGFSKDNNSIITRKFOGKLTFPG 360
DB 301 DMPDILILEIGQFKQTQIIVGVNKDEGTWFLVYGAPGFSKDNNSIITRKFOGKLTFPG 360
QY 361 VSEFGKESILFHYTMDVDPORPENYREALGDVVDNFI CPLAEFTKFSKSGNNAFFYX 420
DB 361 VSEFGKESILFHYTMDVDPORPENYREALGDVVDNFI CPLAEFTKFSKSGNNAFFYX 420
QY 421 FEHRSSKLPMPPEWGMVGHYEIEFVFGPLPERRDNYTKAEIILSRIVKRMANFAKYGNP 480
DB 421 FEHRSSKLPMPPEWGMVGHYEIEFVFGPLPERRDNYTKAEIILSRIVKRMANFAKYGNP 480
QY 481 NETONNSTSWPVFKSTEQKYLILNTBSTIRIMTKLRAQOCRFMTSPFPKYLEMTGNIDAE 540
DB 481 NETONNSTSWPVFKSTEQKYLILNTBSTIRIMTKLRAQOCRFMTSPFPKYLEMTGNIDAE 540
QY 541 MEWKAGFHRMNNYMDWKQFNDYTSKESCVGL 574
DB 541 MEWKAGFHRMNNYMDWKQFNDYTSKESCVGL 574

RESULT 5
ADRO1051
ID ADRO1051 standard; protein; 574 AA.
XX
AC ADRO1051;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/F227A variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOCK J D.
XX
PI Wackins JD, Pancook JD;
XX
XX WPI; 2004-468195/44.
DR N-PSDB; ADRO1050.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
-induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
PS Claim 1; SEQ ID NO 18; 131pp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
NOS: 2-42) or their functional fragments. Also described are: a nucleic
acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416

CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.7%; Score 3102; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.2e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAPPLGRLRFPKQSLTKMSDIMNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAPPLGRLRFPKQSLTKMSDIMNATK 60
QY 61 YANSCCONIDQSPFGHSGEMMNPTDLSBDCLYLWMIIPAPKRNATVLIWYGGGFQT 120
DB 61 YANSCCONIDQSPFGHSGEMMNPTDLSBDCLYLWMIIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFALPGNEAPGNMGLFPQOLALQWVOK 180
DB 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFALPGNEAPGNMGLFPQOLALQWVOK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240
QY 241 NRTLNIAKLTCGSRNEMTEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300
DB 241 NRTLNIAKLTCGSRNEMTEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300
QY 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOBGLKIFPPG 360
DB 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOBGLKIFPPG 360
QY 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYVFCPALEFTYKKSEMGNAFFYY 420
DB 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYVFCPALEFTYKKSEMGNAFFYY 420
QY 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKABEILSRISIVKMANPAKYGNP 480
DB 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKABEILSRISIVKMANPAKYGNP 480
QY 481 NETQNNSTWVPFSTROKTLTNTESIRIMTKLRAQOCRPMTSPFPKVLMTGNDIEAE 540
DB 481 NETQNNSTWVPFSTROKTLTNTESIRIMTKLRAQOCRPMTSPFPKVLMTGNDIEAE 540
QY 541 MEMKAGFHRMNNYMMDMKQFNQDYSKESCVGL 574
DB 541 MEMKAGFHRMNNYMMDMKQFNQDYSKESCVGL 574

RESULT 6
ADRO1035
ID ADRO1035 standard; protein; 574 AA.

XX AC ADRO1035;

XX DT 23-SEP-2004 (first entry)

XX DE Human butyrylcholinesterase A328W/Y332M variant.

XX KM butyrylcholinesterase; cocaine-induced condition;
XX KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
XX KM cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.

OS Synthetic.

XX PN US2004121970-A1.

XX PD 24-JUN-2004.

XX PF 20-DEC-2002; 2002US-00324466.

XX PR 20-DEC-2002; 2002US-00324466.

XX PA (WATK/) WATKINS J D.

XX PA (PANCO/) PANCOCK J D.

XX PI Watkins JD, Pancock JD;

XX DR WPI: 2004-468195/44.

XX DR N-PSDB; ADRO1034.

XX PS Claim 1; SEQ ID NO 2; 133bp; English.

CC The invention describes a butyrylcholinesterase variant polypeptide (1)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (1) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.7%; Score 3102; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.2e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAPPLGRLRFPKQSLTKMSDIMNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAPPLGRLRFPKQSLTKMSDIMNATK 60
QY 61 YANSCCONIDQSPFGHSGEMMNPTDLSBDCLYLWMIIPAPKRNATVLIWYGGGFQT 120
DB 61 YANSCCONIDQSPFGHSGEMMNPTDLSBDCLYLWMIIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFALPGNEAPGNMGLFPQOLALQWVOK 180
DB 121 GTSSLAHYDQKFLARVERVIVSMNYRVGALGFALPGNEAPGNMGLFPQOLALQWVOK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHSLFTRAILQSGSFNAWAATVSYEAR 240
QY 241 NRTLNIAKLTCGSRNEMTEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300
DB 241 NRTLNIAKLTCGSRNEMTEIIKCLRNDPOEILINAEFVVPYGPPLSVNGPTDGPFLT 300
QY 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOBGLKIFPPG 360
DB 301 DMPDILILEQFKKTOILVGNKDEGTWFLVYGAPGSKDNNSIITRKEFOBGLKIFPPG 360
QY 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYVFCPALEFTYKKSEMGNAFFYY 420
DB 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYVFCPALEFTYKKSEMGNAFFYY 420
QY 421 FEHRSSKLPWPEWGVHGYEIEFVGLPLERRDNTYKABEILSRISIVKMANPAKYGNP 480

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Db      421 FEHRSKLPWPEMGMVHGEIEFVGLERRDNTKAEILSRIVKMANPAKYNP 480
Qy      481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRPQQCRFTSPFPKYLEMTGNIDEAE 540
Db      481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRPQQCRFTSPFPKYLEMTGNIDEAE 540
Qy      541 MEMKAGFHRNNNYMMDMKQNFNDYTSKESCVGL 574
Db      541 MEMKAGFHRNNNYMMDMKQNFNDYTSKESCVGL 574

```

RESULT 7

ADRO1041
ID ADRO1041 standard; protein; 574 AA.

AC ADRO1041;

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A328W/Y332S variant.

EE butyrylcholinesterase; cocaine-induced condition;

KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;

KW cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens;

OS Synthetic.

PN US2004121970-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

PR 20-DEC-2002; 2002US-00324466.

PA (WATK/) WATKINS J D.

PA (PANC/) PANCOCK J D.

PI Watkins JD, Pancook JD;

DR WPI, 2004-468195/44.

DR N-PSDB; ADRO1040.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine

PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

PS Claim 1; SEQ ID NO 8; 131bp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (1)

CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID

CC NOS: 2-42) or their functional fragments. Also described are: a nucleic

CC acid encoding (1) comprising any of the 21 nucleic acid sequences of 2416

CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a

CC cocaine-induced condition; and a method of hydrolysing a cocaine-based

CC butyrylcholinesterase substrate. (1) is butyrylcholinesterase variant

CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the

CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The

CC butyrylcholinesterase variant polypeptides and nucleic acids and methods

CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or

CC cocaine addiction. This is the amino acid sequence of a human

CC butyrylcholinesterase variant.

CC Sequence 574 AA;

XX

XX

XX

XX

XX

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Db      1 EDDIIATKNGKVRGMNLTVPGGTVAFLGIPYAPQPLGRLEFKKRPQSLTKNSDIMNATK 60
Qy      61 YANSCCONIDQSPFGTHSGEMNPNPNDLSBDCLYLNWVI PAKPKNATYLIWYGGGFGOT 120
Db      61 YANSCCONIDQSPFGTHSGEMNPNPNDLSBDCLYLNWVI PAKPKNATYLIWYGGGFGOT 120
Qy      121 GTSILHYDCKFLARVERVIVVSMNRYVGLGFLALPGNPEAPGNKGLFDQOLALQWOK 180
Db      121 GTSILHYDCKFLARVERVIVVSMNRYVGLGFLALPGNPEAPGNKGLFDQOLALQWOK 180
Qy      181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHLFTRAIILQSGFPNPMVNTSLYEAR 240
Db      181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHLFTRAIILQSGFPNPMVNTSLYEAR 240
Qy      241 NRTNLAKLTGCSRENETEIIKCLRNKDPQEIILNEAFVVPYGPLSVNFGPTVDDPILT 300
Db      241 NRTNLAKLTGCSRENETEIIKCLRNKDPQEIILNEAFVVPYGPLSVNFGPTVDDPILT 300
Qy      301 DMPDILLELQGFKTQILVGNKDEGTWFLVYGAPGSKUNNSITTRKEFOEGLKIFPPG 360
Db      301 DMPDILLELQGFKTQILVGNKDEGTWFLVYGAPGSKUNNSITTRKEFOEGLKIFPPG 360
Qy      361 VSEFGKESILFHYTDWDDQRPENYREALGDVGVNFCPALFTKKFSEMGNNAFYY 420
Db      361 VSEFGKESILFHYTDWDDQRPENYREALGDVGVNFCPALFTKKFSEMGNNAFYY 420
Qy      421 FEHRSKLPWPEMGMVHGEIEFVGLPLERRDNTKAEILSRIVKMANPAKYNP 480
Db      421 FEHRSKLPWPEMGMVHGEIEFVGLPLERRDNTKAEILSRIVKMANPAKYNP 480
Qy      481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRPQQCRFTSPFPKYLEMTGNIDEAE 540
Db      481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRPQQCRFTSPFPKYLEMTGNIDEAE 540
Qy      541 MEMKAGFHRNNNYMMDMKQNFNDYTSKESCVGL 574
Db      541 MEMKAGFHRNNNYMMDMKQNFNDYTSKESCVGL 574

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RESULT 8

ADRO1037
ID ADRO1037 standard; protein; 574 AA.

AC ADRO1037;

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A328W/Y332P variant.

EE butyrylcholinesterase; cocaine-induced condition;

KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;

KW cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens;

OS Synthetic.

PN US2004121970-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

PR 20-DEC-2002; 2002US-00324466.

PA (WATK/) WATKINS J D.

PA (PANC/) PANCOCK J D.

PI Watkins JD, Pancook JD;

DR WPI, 2004-468195/44.

DR N-PSDB; ADRO1036.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine

PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

PT -induced condition, i. e. cocaine-overdose or cocaine addiction.

PS Claim 1; SEQ ID NO 4; 131pp; English.

CC The invention describes a butyrylcholinesterase-variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolyzing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.

SQ Sequence 574 AA;

Query Match	Score	DB	Length
99.7%	3100	8	574

Matches 573; Conservative 0; Mismatches 1;

Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

XX	Human butyrylcholinesterase mutant A328W.
DE	

KW Human; butyrylcholinesterase; mutant; cocaine hydrolysis
KW cocaine addiction; antiaddictive; antidote; musein.

OS Homo sapiens.
OS Synthetic.

FH	Key	Location/Qualifiers
100		
101		
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103		
104		
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106		
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/note= "wild-type Ala substituted by Trp"

PN WO200264796-A2.

PD 22-AUG-2002
 YX

XX 21-DEC-2001; 2001MO-US050450.

PR	26-DEC-2000; 2000US-00748/39.
PR	20-DEC-2001; 2001US-00032233.

AA
PA
(MOLE-) APPLIED MOLECULAR EVOL

EA (LINE-7) ONLY MEDICINE CENT.
XX

XX 11/11/2023 11:11:11

XX

PT cocaine-induced conditions.

PS Example 1; Page; 150pp; English.

CC The present invention relates to mutants of human butyrylcholinesterase.

CC for treating a cocaine-induced condition. The present sequence is a
CC mutant protein shown in the exemplification of the invention

AA
SQ Sequence 574 AA:

Query Match : 99.6%; Score 3099; DB 5; Length 574;

```

Matches 573; Conservative 0; Mismatches 1;

```

Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	EDDIIILATKNGKVRGMNLTVFGSTVIAFLGI:PYAQPLGRLRFKKPGSLTKMSDIWNA	60
Dp	1	EDDIIILATKNGKVRGMNLTVFGSTVIAFLGI:PYAQPLGRLRFKKPGSLTKMSDIWNA	60
QY	61	YANSCCNINDOSFPGFHGSEMMNPNTLSSECLVLNWTIPAPKPKRNAVLWTIVGGSGQT	120
Dp	61	YANSCCNINDOSFPGFHGSEMMNPNTLSSECLVLNWTIPAPKPKRNAVLWTIVGGSGQT	120
QY	121	GTSSLIHYVDGKFLTARVERVIVVSMNRYVGAALGFLALPGNPEAPGNMGLFDQOLALQWYQK	180
Dp	121	GTSSLIHYVDGKFLTARVERVIVVSMNRYVGAALGFLALPGNPEAPGNMGLFDQOLALQWYQK	180
QY	181	NIAAFGNGPKSVTLFGESAGAAVSLSHLSPGSHSLFTRALLQSGSFPAAPAAVTSLYEAR	240
Dp	181	NIAAFGNGPKSVTLFGESAGAAVSLSHLSPGSHSLFTRALLQSGSFPAAPAAVTSLYEAR	240
QY	241	NRTANLAKLTGSCSRHENETBIIKCLRNDDPOEILINBAFVVYVGGPPLSNFQPTVDDGLYT	300
Dp	241	NRTANLAKLTGSCSRHENETBIIKCLRNDDPOEILINBAFVVYVGGPPLSNFQPTVDDGLYT	300
QY	301	DMPDILLELGQFKKTOILLVGNNDGTFPLVYGA:PGFSKDNNSIITRKEFQEGLKIFPPG	360
Dp	301	DMPDILLELGQFKKTOILLVGNNDGTFPLVYGA:PGFSKDNNSIITRKEFQEGLKIFPPG	360
QY	361	VSEFGKSLIFHYTDWDDQRPENYRRLAGDVGDYNPICALFETKFKFSWGNNAPFY	420
Dp	361	VSEFGKSLIFHYTDWDDQRPENYRRLAGDVGDYNPICALFETKFKFSWGNNAPFY	420

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QY 421 FEHRSKTLPMPEWGMVGHGEIEFVGLPLERRDNTKAEILSRIVKMANFAKYGNP 480
DB 421 FEHRSKTLPMPEWGMVGHGEIEFVGLPLERRDNTKAEILSRIVKMANFAKYGNP 480
QY 481 NETQNNSTWPFVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPKYLEMTGNIDEAE 540
DB 481 NETQNNSTWPFVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPKYLEMTGNIDEAE 540
QY 541 MEWKAGFHRMNNYMDMKNOFNDYTSKKESCVEL 574
DB 541 MEWKAGFHRMNNYMDMKNOFNDYTSKKESCVEL 574

RESULT 10
ADRL049
ID ADRL049 standard; protein; 574 AA.
XX
AC ADRL049;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/S287G/F227A variant.
XX
KM butyrylcholinesterase; cocaine-induced condition;
KM cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.
XX
PA (WATK/) WATKINS J D.
PA (PANCO/) PANCOOK J D.
XX
PI Watkins JD, Pancook JD;
XX
DR WPI: 2004-468195/44.
DR N-PSDB: ADRL01048.
XX
PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
PS Claim 1; SEQ ID NO 16; 131pp; English.
XX
CC The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (II) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (II) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

```

```

DB 1 EDDIIATKNGKVRGMNLTVPFGVTATFLGIPYAPPLGRIRFKKPSLITKMSDIWATK 60
QY 61 YANSCCQNIIDSFPEFHSEMMNPNTDISEDCIYANWIIPAKPKNAATVLIWIGGGFQT 120
DB 61 YANSCCQNIIDSFPEFHSEMMNPNTDISEDCIYANWIIPAKPKNAATVLIWIGGGFQT 120
QY 121 GTSSLHVDGKFLAVERIVVSMNRYVAGLFLALPQNPAPGNGMLFDQOLALQWQK 180
DB 121 GTSSLHVDGKFLAVERIVVSMNRYVAGLFLALPQNPAPGNGMLFDQOLALQWQK 180
QY 181 NIAAFGAPKSVTLFGESAGAAVSLSLHLSPGSHLFTRALIIQSSFNAAPAVLSLYEAR 240
DB 181 NIAAFGAPKSVTLFGESAGAAVSLSLHLSPGSHLFTRALIIQSSGANAAPAVLSLYEAR 240
QY 241 NRTILNAKLTGCSRENETEITKCLNNKPOEILNEAFVPGTPLSYNFGPTVGDGLT 300
DB 241 NRTILNAKLTGCSRENETEITKCLNNKPOEILNEAFVPGTPLSYNFGPTVGDGLT 300
QY 301 DMPDILBELGQFKTQILVGNKDEGTWFLVYGAFGFSKDNNSITTRKEFQGLKIFPPG 360
DB 301 DMPDILBELGQFKTQILVGNKDEGTWFLVYGAFGFSKDNNSITTRKEFQGLKIFPPG 360
QY 361 VSEFGKESILFYHTWVDQREPNYREALGDVVGYNFCPLLETTKFSEGNNAFFY 420
DB 361 VSEFGKESILFYHTWVDQREPNYREALGDVVGYNFCPLLETTKFSEGNNAFFY 420
QY 421 FEHRSKTLPMPEWGMVGHGEIEFVGLPLERRDNTKAEILSRIVKMANFAKYGNP 480
DB 421 FEHRSKTLPMPEWGMVGHGEIEFVGLPLERRDNTKAEILSRIVKMANFAKYGNP 480
QY 481 NETQNNSTWPFVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPKYLEMTGNIDEAE 540
DB 481 NETQNNSTWPFVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSFPKYLEMTGNIDEAE 540
QY 541 MEWKAGFHRMNNYMDMKNOFNDYTSKKESCVEL 574
DB 541 MEWKAGFHRMNNYMDMKNOFNDYTSKKESCVEL 574

RESULT 11
AAE25235
ID AAE25235 standard; protein; 574 AA.
XX
AC AAE25235;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human butyrylcholinesterase protein.
XX
KW Human; optimisation; drug; butyrylcholinesterase; enzyme.
XX
OS Homo sapiens.
XX
FH Key
FH Disulfide-bond 65..92
FT Region
FT Region
FT Active-site 112
FT Active-site 112
FT Active-site 128
FT Active-site 128
FT Region 194..201
FT Region 224..234
FT Active-site 231
FT Disulfide-bond 252..263

```

Region	277. .289	/note= "Region used to generate focussed libraries"
Region	327. .332	/note= "Region used to generate focussed libraries"
Active-site	329	/note= "Aromatic active site gorge residue"
Active-site	332	/note= "Aromatic active site gorge residue"
Disulfide-bond	400. .519	/note= "Region used to generate focussed libraries"
Region	429. .442	/note= "Region used to generate focussed libraries"
Active-site	430	/note= "Aromatic active site gorge residue"
Active-site	440	/note= "Aromatic active site gorge residue"
Active-site	440	/note= "Aromatic active site gorge residue"
MO200244361-A2.		
06-JUN-2002.		
28-NOV-2001; 2001WO-US044600.		
28-NOV-2000; 2000US-00724762.		
(MOLE-) APPLIED MOLECULAR EVOLUTION INC.		
Huse WD;		
WPI; 2002-519586/55.		
New cell composition having population of non-yeast eukaryotic cells		
containing diverse population of variant nucleic acids that are expressed		
in different cell and located within each cell at identical site in		
genome.		
Example 11; Page 155-156; 157pp; English.		
The present invention relates to a cell composition having population of		
non-yeast eukaryotic cells containing a diverse population of ten or more		
variant nucleic acids or heterologous nucleic acid fragments comprising		
distinct species of nucleic acid fragments, each of the variant nucleic		
acids or heterologous nucleic acid fragments being expressed in different		
cells and located within each cell at an identical site in the genome.		
The composition is useful to identify polypeptides exhibiting optimised		
activity. It is also useful for identifying a binding ligand. It is also		
useful for identifying specific ligands to desired target molecules. Such		
ligands can be developed as potential drug candidates or alternatively		
used as lead compounds for the generation and identification of ligand		
variants which exhibit enhanced activity of the desired binding property.		
The methods can similarly be applied to identify a nucleic acid having an		
optimised activity by screening for an activity associated with a parent		
nucleic acid. The present sequence is human butyrylcholinesterase		
protein. This sequence is used in the exemplification of the invention		
Sequence 574 AA;		
Query Match	99.5%;	Score 3096; DB 5; Length 574;
Best Local Similarity	99.8%;	Pred. No. 4.4e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0		
1 EDDIIATKNGKVRGMNLTVFGGTYTAFLGIPYAAPPLGRRLPKKPKQSTTKMSDIWMATK 60		
1 EDDIIATKNGKVRGMNLTVFGGTYTAFLGIPYAAPPLGRRLPKKPKQSTTKMSDIWMATK 60		
YANSCCQNIIDSPFGHSEMMNPNTDISEDCLYTNWMIIPAKPKNAATLTIYGGGFPOT 120		
YANSCCQNIIDSPFGHSEMMNPNTDISEDCLYTNWMIIPAKPKNAATLTIYGGGFPOT 120		
GTSSLIHVVDGKFLAVERITYVSNMYRVRGALGFLALPGNPEAPGMNGLFDQDLALQWQK 180		
GTSSLIHVVDGKFLAVERITYVSNMYRVRGALGFLALPGNPEAPGMNGLFDQDLALQWQK 180		
181 NIAPFGNPKSVTLTFGESAGAAVSILHLISPCSHSLFTRAILIQSGSFNAPMAVTSLYEAR 240		

Dd	181	NIAAFQGNKSYTLTGESAGAAVSJLHLSGSHSLFTRALJOGSFRNAPAAVTSJYEAR	2400
Qy	241	NRTLANLAKTGCSRENETETIKCLANKDPOEILNEAFVPEYGTPLSVNFPTVDGFLT	3000
Dd	241	NRTLANLAKTGCSRENETETIKCLANKDPOEILNEAFVPEYGTPLSVNFPTVDGFLT	3000
Qy	301	DMDLILLEGOFKKTQILVGVNKDEGTFVLVYGAPGSKDNNSITTRKEFOEGLKIFPPG	3600
Dd	301	DMDLILLEGOFKKTQILVGVNKDEGTFVLVYGAPGSKDNNSITTRKEFOEGLKIFPPG	3600
Qy	361	VSEFGKESILFHYTDMVDDQRPENRREALGDVVDYNFICPALEFTYKFSBKGNAFFYY	4200
Dd	361	VSEFGKESILFHYTDMVDDQRPENRREALGDVVDYNFICPALEFTYKFSBKGNAFFYY	4200
Qy	421	FEHRSKTLPMPEMGVMGHEIEIEFYGLPERRDNYTKAEIISRSJLYKMANPAKYGNP	4800
Dd	421	FEHRSKTLPMPEMGVMGHEIEIEFYGLPERRDNYTKAEIISRSJLYKMANPAKYGNP	4800
Qy	481	NETONNSTMPPEKSTEOCYLLTNESRINTYKLAQOOCRWTSFPFKULBMTGNIDEAE	5400
Dd	481	NETONNSTMPPEKSTEOCYLLTNESRINTYKLAQOOCRWTSFPFKULBMTGNIDEAE	5400
Qy	541	MEWKAGFHRNNNYMDMKQOFNDYTSKKESCJGL	574
Dd	541	MEWKAGFHRNNNYMDMKQOFNDYTSKKESCJGL	574

	RESULT 12
ID	AAO18982
ID	MAOI8982 standard; protein; 574 AA.
XX	
AC	AAO18982;
XX	
DY	02-DEC-2002 (first entry)
XX	
DE	Human butyrylcholinesterase mutant A328/V331L.
XX	
KW	Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis; cocaine addiction; antididictive; antidote; mutein.
KX	
OS	Homo sapiens.
OS	Synthetic.
XK	
FH	Key Location/Qualifiers
FT	Misc-difference 328
FT	/note= "wild-type Ala substituted by Trp"
FT	Misc-difference 331
FT	/note= "wild-type Val substituted by Leu"
NN	
NN	WO200264796-A2.
PD	
PD	22-AUG-2002.
XX	
PF	21-DEC-2001; 2001MO-US050450.
XX	
FR	26-DEC-2000; 2000US-00748739.
XX	
FR	20-DEC-2001; 2001US-00032233.
PA	(MOL-B-) APPLIED MOLECULAR EVOLUTION INC. (UTNE-) UNIV NEBRASKA MEDICAL CENT.
PI	
PL	Lockridge O., Watkins JD., Pancook DJ;
DR	WPI; 2002-636633/68.
XX	
PT	New human butyrylcholinesterase variant polypeptides, useful for treating cocaine-induced conditions.
XX	
PS	Claim 1; Page; 150pp; English.
CC	The present invention relates to mutants of human butyrylcholinesterase. The enzymes have an increased cocaine hydrolisis activity and can be used

CC for treating a cocaine-induced condition. The present sequence is a
CC mutant protein shown in the exemplification of the invention

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;
Best Local Similarity 99.7%; Pred. No. 4.4e-277;
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLRFRKPKQSLTKMSDINMNTK 60
   |||||||
DB 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLRFRKPKQSLTKMSDINMNTK 60
QY 61 YANSCCNDIOSFPFGHSEMMNPTDLSBDCLYANWIPAPKRNATVLIWYGGGFQT 120
   |||||||
DB 61 YANSCCNDIOSFPFGHSEMMNPTDLSBDCLYANWIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLHYVDGKFLARVERIVVSMNRYVAGLGLALPQNPAPGNMGLFDQQLALQWVOK 180
   |||||||
DB 121 GTSSLHYVDGKFLARVERIVVSMNRYVAGLGLALPQNPAPGNMGLFDQQLALQWVOK 180
QY 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
   |||||||
DB 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
QY 241 NRTLNLAULTGCSRENETEIIKCLRNKDPQEIILNEAFVVPYGTPLSVNFGPTVDGDFLT 300
   |||||||
DB 241 NRTLNLAULTGCSRENETEIIKCLRNKDPQEIILNEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILILEGQFKTKQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGIKIFPPG 360
   |||||||
DB 301 DMPDILILEGQFKTKQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGIKIFPPG 360
QY 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYFNFCPALFTKFSWGNNAFFYY 420
   |||||||
DB 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYFNFCPALFTKFSWGNNAFFYY 420
QY 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANPAKYNP 480
   |||||||
DB 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANPAKYNP 480
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOOCRFWTSFPFKYLEMTGNIDAE 540
   |||||||
DB 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOOCRFWTSFPFKYLEMTGNIDAE 540
QY 541 MEMKAGFHRNNNYMDWKQNFNDYTSKESCVGL 574
   |||||||
DB 541 MEMKAGFHRNNNYMDWKQNFNDYTSKESCVGL 574

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RESULT 13

AAO18898 standard; protein; 574 AA.

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XX AAO18898
XX
XX AAO18898;
XX
XX 02-DEC-2002 (first entry)
XX
XX Human butyrylcholinesterase.
XX
XX Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
XX cocaine addiction; antiaddictive; antidote.
XX
XX Homo sapiens.
XX
XX WO200264796-A2.
XX
XX 22-AUG-2002.
XX
XX 21-DEC-2001; 2001MO-US050450.
XX
XX 26-DEC-2000; 2000US-00748739.
XX
XX 20-DEC-2001; 2001US-00032233.
XX

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XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.

PA (UNNE-) UNIV NEBRASKA MEDICAL CENT.

XX Lockridge O, Watkins JD, Pancook JD;

XX WPI, 2002-636633/68.

PT New human butyrylcholinesterase variant polypeptides, useful for treating
PT cocaine-induced conditions.

PS Example 3; Fig 2; 150bp; English.

CC The present invention relates to mutants of human butyrylcholinesterase.
CC The enzymes have an increased cocaine hydrolysis activity and can be used
CC for treating a cocaine-induced condition. The present sequence is a
CC protein shown in the exemplification of the invention

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.4e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLRFRKPKQSLTKMSDINMNTK 60
   |||||||
DB 1 EDDIIITKNGKVRGMNLTVEGGVTAFGLGIPYAPPLGRLRFRKPKQSLTKMSDINMNTK 60
QY 61 YANSCCNDIOSFPFGHSEMMNPTDLSBDCLYANWIPAPKRNATVLIWYGGGFQT 120
   |||||||
DB 61 YANSCCNDIOSFPFGHSEMMNPTDLSBDCLYANWIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLHYVDGKFLARVERIVVSMNRYVAGLGLALPQNPAPGNMGLFDQQLALQWVOK 180
   |||||||
DB 121 GTSSLHYVDGKFLARVERIVVSMNRYVAGLGLALPQNPAPGNMGLFDQQLALQWVOK 180
QY 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
   |||||||
DB 181 NIAAFGKPKSVTLFGESAGASVSLHLSFGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
QY 241 NRTLNLAULTGCSRENETEIIKCLRNKDPQEIILNEAFVVPYGTPLSVNFGPTVDGDFLT 300
   |||||||
DB 241 NRTLNLAULTGCSRENETEIIKCLRNKDPQEIILNEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILILEGQFKTKQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGIKIFPPG 360
   |||||||
DB 301 DMPDILILEGQFKTKQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGIKIFPPG 360
QY 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYFNFCPALFTKFSWGNNAFFYY 420
   |||||||
DB 361 VSEFGKESILFHYTDWVDORPENYREALGDVVDYFNFCPALFTKFSWGNNAFFYY 420
QY 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANPAKYNP 480
   |||||||
DB 421 FEHRSSKLPWPMWGVHGYEIEFVFGPLERRDNTYKAEELISRSIVKRWANPAKYNP 480
QY 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOOCRFWTSFPFKYLEMTGNIDAE 540
   |||||||
DB 481 NETONNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOOCRFWTSFPFKYLEMTGNIDAE 540
QY 541 MEMKAGFHRNNNYMDWKQNFNDYTSKESCVGL 574
   |||||||
DB 541 MEMKAGFHRNNNYMDWKQNFNDYTSKESCVGL 574

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RESULT 14

ABR62391 standard; protein; 574 AA.

```

XX ABR62391
XX
XX ABR62391;
XX
XX 03-OCT-2003 (first entry)
XX

```

DE Human butyrylcholinesterase.
 XX Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;
 KM EC-3.1.1.8.
 XX Homo sapiens.
 PN MO2003054182-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 19-DEC-2002; 2002MO-IB005526.
 XX
 PR 21-DEC-2001; 2001US-0344295P.
 XX
 PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.
 PI Karatzae C, Huang Y, Lazaris A;
 XX
 DR WPI; 2003-559148/52.
 XX
 DR N-PDB; ACC84169.
 XX
 PT New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase
 PT (Bche) enzyme in its milk or urine, useful for large-scale production of
 PT recombinant BChE to prevent or treat organophosphate poisoning or cocaine
 PT intoxication.
 XX
 PS Claim 10; Page 100-102; 112pp; English.
 XX
 CC The present sequence is the protein sequence of human
 CC butyrylcholinesterase (BChE). The invention provides methods for large-
 CC scale production of recombinant BChE in cell culture, and in the milk
 CC and/or urine of transgenic mammals. The genome of the transgenic mammal
 CC (e.g. goat) comprises a DNA sequence that encodes BChE operably linked to
 CC a mammary gland-specific promoter or to a urinary endothelium-specific
 CC promoter, and a signal sequence that provides secretion of the BChE
 CC enzyme into the milk or urine of the mammal. The recombinant BChE can be
 CC used in preventing and/or treating organophosphate pesticide poisoning,
 CC nerve gas poisoning, cocaine intoxication or succinylcholine-induced
 CC apnoea
 CC
 SQ Sequence 574 AA;
 Query Match 99.5%; Score 3096; DB 6; Length 574;
 Best Local Similarity 99.8%; Pred. No. 4.4e-277;
 Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EDDIIATKNGKVRGNNLTVFGGTVAFLGIPIYAOPPLGRLRFKKQSLTKMSDINWATK 60
 DB 1 EDDIIATKNGKVRGNNLTVFGGTVAFLGIPIYAOPPLGRLRFKKQSLTKMSDINWATK 60
 QY 61 YAASCCNINQSPFGFSGEMWNPNTDLSDCLYIANWIPAPKXKATVLIWYGGGFOT 120
 DB 61 YAASCCNINQSPFGFSGEMWNPNTDLSDCLYIANWIPAPKXKATVLIWYGGGFOT 120
 QY 121 GTSSLAHYDQKFLARVERVIVSNVYRVALGFLALPGNPEAPGNMGLPQOQLALQWOK 180
 DB 121 GTSSLAHYDQKFLARVERVIVSNVYRVALGFLALPGNPEAPGNMGLPQOQLALQWOK 180
 QY 181 NIAAFGNGNPKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAFWAVTSLEYAR 240
 DB 181 NIAAFGNGNPKSVTLFGESAGAAVSILHLSPGSHSLFTRAILQSGSFNAFWAVTSLEYAR 240
 QY 241 NRTLTNLAKLTCGCRENTEIILKLRNDPOEILINAEFVVPYGPPLSVNGPTVDGPILT 300
 DB 241 NRTLTNLAKLTCGCRENTEIILKLRNDPOEILINAEFVVPYGPPLSVNGPTVDGPILT 300
 QY 301 DMEDILLETGQPKKTQILVGNKDEGTWPLVYGAPGSKNNNSIITRKEQEGKXIFPG 360
 DB 301 DMEDILLETGQPKKTQILVGNKDEGTWPLVYGAPGSKNNNSIITRKEQEGKXIFPG 360
 QY 361 VSEFGKESILFHYTDWVDQRPENYREALGDVVDYVFCPALEFTTKFSWGNNAFFYY 420
 DB 361 VSEFGKESILFHYTDWVDQRPENYREALGDVVDYVFCPALEFTTKFSWGNNAFFYY 420

DB 361 VSEFGKESILFHYTDWVDQRPENYREALGDVVDYVFCPALEFTTKFSWGNNAFFYY 420
 QY 421 FEHRSSKLPWEMWGMHGEIEFVGLPLERDNTKAEILSRSIVKRWANPAKXGNP 480
 DB 421 FEHRSSKLPWEMWGMHGEIEFVGLPLERDNTKAEILSRSIVKRWANPAKXGNP 480
 QY 481 NETQNNSTWVPVKSTEQKYLTLNTESTRIIMTKLRQOQCFWTSFPPKYLEMTGNIDEAR 540
 DB 481 NETQNNSTWVPVKSTEQKYLTLNTESTRIIMTKLRQOQCFWTSFPPKYLEMTGNIDEAR 540
 QY 541 MEWKAGFHRNNNMMDKNOFNDYTSKESCVGL 574
 DB 541 MEWKAGFHRNNNMMDKNOFNDYTSKESCVGL 574
 RESULT 15
 ID AEM00695 standard; protein; 574 AA.
 XX
 AC AEM00695;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX Human butyrylcholinesterase protein.
 DE Human butyrylcholinesterase protein.
 XX
 KM Human; butyrylcholinesterase; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase"
 FT 82
 FT Active-site
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 110..121
 FT Region
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase"
 FT 112
 FT Active-site
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 128
 FT Region
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase"
 FT 194..201
 FT Region
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase"
 FT 224..234
 FT Region
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 231
 FT Active-site
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 277..289
 FT Region
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 327..332
 FT Region
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 429..442
 FT Active-site
 FT /note= "Region used to generate focused libraries of
 FT butyrylcholinesterase variants"
 FT 430
 FT Active-site
 FT 440
 XX
 PN US2003096401-A1.
 PD 22-MAY-2003.
 XX
 PF 28-NOV-2001; 2001US-00997209.
 XX
 PR 28-NOV-2000; 2000US-0367370P.
 XX
 PA (HUSE/) HUSE W D.
 XX
 PI Huse WD;
 XX
 DR WPI; 2003-786991/74.

XX Cell composition comprises non-yeast eukaryotic cells having diverse
PT population of variant nucleic acids or heterologous nucleic acid
XX fragments, useful for identifying polypeptide with optimized activity.
XX
XX Example 11; Fig 8; Opp; English.

XX The invention relates to a cell composition comprising a population of
CC non-yeast eukaryotic cells containing diverse population of variant
CC nucleic acids, or heterologous nucleic acid fragments with distinct
CC species of nucleic acid fragments, where each of the variant nucleic
CC acids or heterologous nucleic acid fragments are expressed in different
CC cell and located within each cell at an identical site in the genome. The
CC invention is useful for identifying polypeptide with optimized activity
CC and for identifying a polypeptide receptor for a ligand. The present
CC sequence is human butyrylcholinesterase protein. This sequence is used in
CC the exemplification of the invention

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 7; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.4e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAPPLRLRFPKQSLTKMSDINWATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAPPLRLRFPKQSLTKMSDINWATK 60
QY 61 YANSCCONIDOSPFGHSGEMNPNPTDLSBDCILYNWIPAPKRNATVLIWYGGGFQT 120
DB 61 YANSCCONIDOSPFGHSGEMNPNPTDLSBDCILYNWIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLHAYVDGKFLARVERVIVSMNRYVAGLGFALPBNPAPGNMGLFDQQLALQWVOK 180
DB 121 GTSSLHAYVDGKFLARVERVIVSMNRYVAGLGFALPBNPAPGNMGLFDQQLALQWVOK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIILOGSGFNAPWATVSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIILOGSGFNAPWATVSLYEAR 240
QY 241 NRTNLAKITGCSRENTEIILKLRNDPOEIIINEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTNLAKITGCSRENTEIILKLRNDPOEIIINEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILLEGOFKKTQIILGVNKGDTWFLVYGAPGSKNNNSITTRKEPQGLKIFPPG 360
DB 301 DMPDILLEGOFKKTQIILGVNKGDTWFLVYGAPGSKNNNSITTRKEPQGLKIFPPG 360
QY 361 VSEFGKESILFHYTDVDDQRPENYREALGVGVNFCPALBETKKESEWGNNAFFY 420
DB 361 VSEFGKESILFHYTDVDDQRPENYREALGVGVNFCPALBETKKESEWGNNAFFY 420
QY 421 FEHRSKSLPMPWEMGVAGYEIEFVGLPDERDNTYKAEILSRISYKRNANPKYGNP 480
DB 421 FEHRSKSLPMPWEMGVAGYEIEFVGLPDERDNTYKAEILSRISYKRNANPKYGNP 480
QY 481 NETQNNSTWPKVSKTEOKYLTINTSESTRIMTKLRNQOCCRFWTSFPFKLEMTGIDBAE 540
DB 481 NETQNNSTWPKVSKTEOKYLTINTSESTRIMTKLRNQOCCRFWTSFPFKLEMTGIDBAE 540
QY 541 WEWKAQFHRNNNTMMKNOFNDYTSKESCVGL 574
DB 541 WEWKAQFHRNNNTMMKNOFNDYTSKESCVGL 574

RESULT 16
ADP44639
ID ADP44639 standard; protein; 574 AA.
AC ADP44639;
XX
DT 09-SEP-2004 (first entry)
XX

DE Human butyrylcholinesterase wild-type protein.

XX butyrylcholinesterase, cytosolic; metastatic colorectal cancer; ovarian;
XX lung; non-Hodgkin's lymphoma; gene therapy; human; wild-type; enzyme.
XX
XX Homo sapiens.

PH Key Location/Qualifiers
FT Disulfide-bond 65..92
FT Disulfide-bond /label = Disulphide_bond
FT Disulfide-bond 252..263
FT Disulfide-bond /label = Disulphide_bond
FT Disulfide-bond 400..519
FT Disulfide-bond /label = Disulphide_bond

PN WO2004050041-A2.

PD 17-JUN-2004.

PF 04-DEC-2003; 2003WO-US038684.

PK 04-DEC-2002; 2002US-00310666.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.

PI Watkins JD, Pancook JD;

DR WPI; 2004-460989/43.

XX N-PSDB; ADP44638.

XX New butyrylcholinesterase variant or functional fragment useful for
PT treating cancer, e.g. metastatic colorectal cancer, ovarian cancer, lung
PT cancer or non-Hodgkin's lymphoma.

XX Example 1; SEQ ID NO 22; 123pp; English.

XX The invention relates to a novel butyrylcholinesterase variant comprising
CC an amino acid sequence selected from any given in the specification, or
CC its functional fragment. The variant of the invention demonstrates
CC cytosolic activity and may be useful for treating cancer, particularly
CC metastatic colorectal cancer, ovarian cancer, lung cancer or non-
CC Hodgkin's lymphoma, possibly via gene therapy. The current sequence is
CC that of the human butyrylcholinesterase wild-type protein of the
CC invention.

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.4e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAPPLRLRFPKQSLTKMSDINWATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAPPLRLRFPKQSLTKMSDINWATK 60
QY 61 YANSCCONIDOSPFGHSGEMNPNPTDLSBDCILYNWIPAPKRNATVLIWYGGGFQT 120
DB 61 YANSCCONIDOSPFGHSGEMNPNPTDLSBDCILYNWIPAPKRNATVLIWYGGGFQT 120
QY 121 GTSSLHAYVDGKFLARVERVIVSMNRYVAGLGFALPBNPAPGNMGLFDQQLALQWVOK 180
DB 121 GTSSLHAYVDGKFLARVERVIVSMNRYVAGLGFALPBNPAPGNMGLFDQQLALQWVOK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIILOGSGFNAPWATVSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTFRAIILOGSGFNAPWATVSLYEAR 240
QY 241 NRTNLAKITGCSRENTEIILKLRNDPOEIIINEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTNLAKITGCSRENTEIILKLRNDPOEIIINEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILLEGOFKKTQIILGVNKGDTWFLVYGAPGSKNNNSITTRKEPQGLKIFPPG 360
DB 301 DMPDILLEGOFKKTQIILGVNKGDTWFLVYGAPGSKNNNSITTRKEPQGLKIFPPG 360

Db 301 DMPDILLELGQFKKTQLLVGVNKGDTAFLVYGAPGFSKDNNSITTRKEFOEGLKIFPPG 360
 QY 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSEMGNNAPFY 420
 Db 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSEMGNNAPFY 420
 QY 421 FEHRSSKLPMPBMWGVHGYEIEFVFGPLPERDNYTKAEIISRSIVKMANPAKYGNP 480
 Db 421 FEHRSSKLPMPBMWGVHGYEIEFVFGPLPERDNYTKAEIISRSIVKMANPAKYGNP 480
 QY 481 NETONNSTSWPVFKSTQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDAE 540
 Db 481 NETONNSTSWPVFKSTQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDAE 540
 QY 541 MEWKAGFHRMNNYMMDMKQNFNDYTSKKESCVEL 574
 Db 541 MEWKAGFHRMNNYMMDMKQNFNDYTSKKESCVEL 574

RESULT 17

ADRO1077
 ID ADRO1077 standard; protein; 574 AA.

AC ADRO1077;
 DT 23-SEP-2004 (first entry)
 XX
 DE Human butyrylcholinesterase.

XX butyrylcholinesterase; cocaine-induced condition;
 KM cocaine-passed butyrylcholinesterase substrate; cocaine-overdose;
 KM cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.

XX US2004121970-A1.

XX 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

XX 20-DEC-2002; 2002US-00324466.

PA (WATK/) WATKINS J D.
 PA (PANC/) PANCOCK J D.

PI Watkins JD, Pancook JD;

XX WPI; 2004-468195/44.

DR N-PSDB; ADRO1076.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
 PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

XX Disclosure; SEQ ID NO 44; 131bp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)
 CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
 CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
 CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
 CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
 CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
 CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
 CC polypeptide comprising any of the 21 sequences of 57 amino acids each
 CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
 CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
 CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
 CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
 CC cocaine addiction. This is the amino acid sequence of human
 CC butyrylcholinesterase.

XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 8; Length 574;
 Best Local Similarity 99.8%; Pred. No. 4.4e-277;
 Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIITKKGKRGMLATFGGVTAPFLGIPAPQAPLGLRFPKPSLTKMSDINATK 60
 Db 1 EDDIIITKKGKRGMLATFGGVTAPFLGIPAPQAPLGLRFPKPSLTKMSDINATK 60
 QY 61 YANSCCONIDQSPFGFHSSEMMNPNTDLSBDCYLANWIMAPKKNATVIMWGGGFGQT 120
 Db 61 YANSCCONIDQSPFGFHSSEMMNPNTDLSBDCYLANWIMAPKKNATVIMWGGGFGQT 120
 QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPBAPGNMGLPQOALQWVOK 180
 Db 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNPBAPGNMGLPQOALQWVOK 180
 QY 181 NIAAFGNPNSVTLFGSSAGASVSLHLSPGSHSLFTRAILLOSGSFNAAPAVTSLYEAR 240
 Db 181 NIAAFGNPNSVTLFGSSAGASVSLHLSPGSHSLFTRAILLOSGSFNAAPAVTSLYEAR 240
 QY 241 NRTLNIAKLTCGSRNETETIICKLRNDPOEILNBAFVVPYGTPLSVNFGPTVDGDFLT 300
 Db 241 NRTLNIAKLTCGSRNETETIICKLRNDPOEILNBAFVVPYGTPLSVNFGPTVDGDFLT 300
 QY 301 DMPDILLELGQFKKTQLLVGVNKGDTAFLVYGAPGFSKDNNSITTRKEFOEGLKIFPPG 360
 Db 301 DMPDILLELGQFKKTQLLVGVNKGDTAFLVYGAPGFSKDNNSITTRKEFOEGLKIFPPG 360
 QY 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSEMGNNAPFY 420
 Db 361 VSEFGKESILFHTYDWDQDQRPENYREALGDVGDVNFICPALBFTKKFSEMGNNAPFY 420
 QY 421 FEHRSSKLPMPBMWGVHGYEIEFVFGPLPERDNYTKAEIISRSIVKMANPAKYGNP 480
 Db 421 FEHRSSKLPMPBMWGVHGYEIEFVFGPLPERDNYTKAEIISRSIVKMANPAKYGNP 480
 QY 481 NETONNSTSWPVFKSTQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDAE 540
 Db 481 NETONNSTSWPVFKSTQKYLTLNTESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDAE 540
 QY 541 MEWKAGFHRMNNYMMDMKQNFNDYTSKKESCVEL 574
 Db 541 MEWKAGFHRMNNYMMDMKQNFNDYTSKKESCVEL 574

RESULT 18

AAY59235
 ID AAY59235 standard; protein; 602 AA.

AC AAY59235;

DT 27-MAR-2000 (first entry)

XX Human butyryl cholinesterase (BuChE) mutant.

XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
 KM butyrylcholinesterase; BuChE; carboxylesterase; GAB; sheep dip; human;
 KM nerve agent; organophosphorus acid anhydride; OPA; mutant.

OS Homo sapiens.

XX Synthetic.

PN US6001625-A.

XX 14-DEC-1999.

XX 19-MAY-1995; 95US-00446100.

PR 19-MAY-1995; 95US-00446100.

PA (USSA) US SEC OF ARMY.

PI Broomfield CA, Lockridge O, Millard CB;

XX MPI, 2000-096137/08.

XX Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.

XX Disclosure; Col 99-102; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CAE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

99.5%; Score 3096; DB 3; Length 602;

Query Match Best Local Similarity 99.8%; Pred. No. 4.7e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

1 EDDIIITKNGKVRGMNLTVEGVTAFGLIPYAPPLGRFRKKPQSLTKMSDINWATK 60
29 EDDIIITKNGKVRGMNLTVEGVTAFGLIPYAPPLGRFRKKPQSLTKMSDINWATK 88
61 YANSCCONIDOSFPGFSGEMNPNNTDLSBDCLYLWVWPAPKRNATVLIWYGGGFGT 120
89 YANSCCONIDOSFPGFSGEMNPNNTDLSBDCLYLWVWPAPKRNATVLIWYGGGFGT 148
121 GTSSLHYVDGKFLARVERVIVSMNRYVAGLFLALPGNPEAPGMGLFDQQLALQWVK 180
149 GTSSLHYVDGKFLARVERVIVSMNRYVAGLFLALPGNPEAPGMGLFDQQLALQWVK 208
181 NIAAFGNGKSVTLFGESAGAAVSILHLSFGSHSLFTRAILQSGSFNAPMAVTSIYEAR 240
209 NIAAFGNGKSVTLFGESAGAAVSILHLSFGSHSLFTRAILQSGSFNAPMAVTSIYEAR 268
241 NRTIANLAKITGCSRENTEI IKLRNKDPOEILNEAFVVPYGPVSVNFGPTVDGDLT 300
269 NRTIANLAKITGCSRENTEI IKLRNKDPOEILNEAFVVPYGPVSVNFGPTVDGDLT 328
301 DMPDILLLEIGQFKKTOIIVGNKDEBTWFLVYGAPEFSKDNNSITTRKEFGGLKIFPPG 360
329 DMPDILLLEIGQFKKTOIIVGNKDEBTWFLVYGAPEFSKDNNSITTRKEFGGLKIFPPG 388
361 VSEFGKESILFHTDWDDORPENYREALGVVGNFICPALFETKKESEWGNNAFFY 420
389 VSEFGKESILFHTDWDDORPENYREALGVVGNFICPALFETKKESEWGNNAFFY 448
421 FEHRSKLPWPEWNGVNGEIEFVFGPLERDNTTKABELLSRIVRWANPAKYGP 480
449 FEHRSKLPWPEWNGVNGEIEFVFGPLERDNTTKABELLSRIVRWANPAKYGP 508
481 NETONNSTSWPVFSTEOKTLTINTESTRTMTKLRAQOCFTSFPPKYLEMTGNIDEAE 540
509 NETONNSTSWPVFSTEOKTLTINTESTRTMTKLRAQOCFTSFPPKYLEMTGNIDEAE 568
541 WEMKAGFRMNNYMMQNOFNDYTSKESCVGL 574
569 WEMKAGFRMNNYMMQNOFNDYTSKESCVGL 602

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AAI94971
ID AAI94971 standard; protein; 602 AA.

XX AAI94971;

XX 27-MAR-2000 (first entry)

XX Human wild-type butyryl cholinesterase (BuChE).

XX Organophosphate, detoxification; esterase; acetylcholinesterase; AChE;
XX butyrylcholinesterase; BuChE; carboxylesterase; CAE; sheep dip; human;
XX nerve agent; organophosphorus acid anhydride; OPAA.

XX Homo sapiens.

XX US6001625-A.

XX 14-DEC-1999.

XX 19-MAY-1995; 95US-00446100.

XX 19-MAY-1995; 95US-00446100.

XX (USSA) US SEC OF ARMY.

XX Broomfield CA, Lockridge O, Millard CB;

XX MPI, 2000-096137/08.

XX Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.

XX Disclosure; Col 3-4; 64pp; English.

XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butyrylcholinesterases (BuChE) and/or carboxylesterases (CAE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CAE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA

XX Sequence 602 AA;

Query Match Best Local Similarity 99.8%; Score 3096; DB 3; Length 602;

Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

1 EDDIIITKNGKVRGMNLTVEGVTAFGLIPYAPPLGRFRKKPQSLTKMSDINWATK 60
29 EDDIIITKNGKVRGMNLTVEGVTAFGLIPYAPPLGRFRKKPQSLTKMSDINWATK 88
61 YANSCCONIDOSFPGFSGEMNPNNTDLSBDCLYLWVWPAPKRNATVLIWYGGGFGT 120
89 YANSCCONIDOSFPGFSGEMNPNNTDLSBDCLYLWVWPAPKRNATVLIWYGGGFGT 148
121 GTSSLHYVDGKFLARVERVIVSMNRYVAGLFLALPGNPEAPGMGLFDQQLALQWVK 180
149 GTSSLHYVDGKFLARVERVIVSMNRYVAGLFLALPGNPEAPGMGLFDQQLALQWVK 208
181 NIAAFGNGKSVTLFGESAGAAVSILHLSFGSHSLFTRAILQSGSFNAPMAVTSIYEAR 240
209 NIAAFGNGKSVTLFGESAGAAVSILHLSFGSHSLFTRAILQSGSFNAPMAVTSIYEAR 268

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QY 241 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGFPTVDGDFLT 300
 DB 269 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGFPTVDGDFLT 328
 QY 301 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPQEGKIFPPG 360
 DB 329 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPQEGKIFPPG 388
 QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFTKKFSWGNNAFFYY 420
 DB 389 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFTKKFSWGNNAFFYY 448
 QY 421 FEHRSSKLPWPEWVGWVGVEIEFVFGPLPERDNYTKAEIISRSIVKRWANPAKYGNP 480
 DB 449 FEHRSSKLPWPEWVGWVGVEIEFVFGPLPERDNYTKAEIISRSIVKRWANPAKYGNP 508
 QY 481 NETONNSTSWPVFSTQKTLTNTSESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDBAE 540
 DB 509 NETONNSTSWPVFSTQKTLTNTSESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDBAE 568
 QY 541 MEWKAGFHRNNNYMDWKQNFNDYTSKKESCVEL 574
 DB 569 MEWKAGFHRNNNYMDWKQNFNDYTSKKESCVEL 602

RESULT 20

AAY44573
 ID AAY44573 standard; protein; 602 AA.

AAV44573;

04-APR-2000 (first entry)

Human wild type Butyrylcholinesterase (BChE) protein.

Butyrylcholinesterase; BChE allele; neurological disease; treatment;
 therapy; allelic variant; BChE-K; apoE4 allele; neurofibromatosis;
 non-AD neurological disease; Alzheimer's disease; Huntington's disease;
 depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
 Parkinson's disease; multi-infarct dementia; human.

Homo sapiens.

MO9966072-A2.

23-DEC-1999.

16-JUN-1999; 99MO-IB001298.

16-JUN-1998; 98US-0089406P.

(NOVA-) NOVA MOLECULAR INC.

Seviigny P, Wiebusch H, Schappert K;

WPI; 2000-126550/11.

N-PSDB; AAZ49470.

Prediction of drug efficacy for treating neurological diseases like

Alzheimer's disease, neurofibromatosis, Huntington's disease.

Example 1; Fig 3; 37pp; English.

The present sequence is the wild type human butyrylcholinesterase (BChE)
 protein. Determining BChE allele status of a patient helps predicting
 risk for neurological diseases, efficacy of therapy and determining
 treatment protocol. Presence of BChE allelic variant, BChE-K and apoE4
 allele indicate patient's risk for having a neurological disease. This
 method enables treating Alzheimer's disease, depression,
 neurofibromatosis, Huntington's disease, amyotrophic lateral sclerosis,
 multiple sclerosis, stroke, Parkinson's disease, multi-infarct dementia
 and other non-AD neurological diseases

Sequence 602 AA;

Query Match 99.5%; Score 3096; DB 3; Length 602;

Best Local Similarity 99.8%; Pred. No. 4,7e-277;

Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGNMLTVFGGTVAFLGIPIYAQPELGLRFRKKPOSTLRKSDIWNATK 60
 DB 29 EDDIIATKNGKVRGNMLTVFGGTVAFLGIPIYAQPELGLRFRKKPOSTLRKSDIWNATK 88
 QY 61 YANSCCNIDQSPFGFGSEMMNPNDLSBDCYLWNWIPAPKXKATVLIWYGGGFQT 120
 DB 89 YANSCCNIDQSPFGFGSEMMNPNDLSBDCYLWNWIPAPKXKATVLIWYGGGFQT 148
 QY 121 GTSLSHYDQKFLARVERVIVSMNRYVAGLGFALPGNBEAPGNMGLFQOQLAQWVK 180
 DB 149 GTSLSHYDQKFLARVERVIVSMNRYVAGLGFALPGNBEAPGNMGLFQOQLAQWVK 208
 QY 181 NIAAFGNPKSVTLFGESAGAAVSJHLSPGSHSLFTRAILQSGSFNAFMAVTSIYEAR 240
 DB 209 NIAAFGNPKSVTLFGESAGAAVSJHLSPGSHSLFTRAILQSGSFNAFMAVTSIYEAR 268
 QY 241 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGFPTVDGDFLT 300
 DB 269 NRTLNIAKLTCGSRNETEIIKCLRNDPOEIIINAEFVVPYGTPLSVNGFPTVDGDFLT 328
 QY 301 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPQEGKIFPPG 360
 DB 329 DMPDILLELQPKKTOILVGNKDEGTWFLVYGAPGSKNNSTITRKEPQEGKIFPPG 388
 QY 361 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFTKKFSWGNNAFFYY 420
 DB 389 VSEFGKESILFHYTDWDDORPENYREALGDVVDYNYFCPALFTKKFSWGNNAFFYY 448
 QY 421 FEHRSSKLPWPEWVGWVGVEIEFVFGPLPERDNYTKAEIISRSIVKRWANPAKYGNP 480
 DB 449 FEHRSSKLPWPEWVGWVGVEIEFVFGPLPERDNYTKAEIISRSIVKRWANPAKYGNP 508
 QY 481 NETONNSTSWPVFSTQKTLTNTSESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDBAE 540
 DB 509 NETONNSTSWPVFSTQKTLTNTSESTRIMTKLRAOQCRFWTSFPFKVLEMTGNIDBAE 568
 QY 541 MEWKAGFHRNNNYMDWKQNFNDYTSKKESCVEL 574
 DB 569 MEWKAGFHRNNNYMDWKQNFNDYTSKKESCVEL 602

RESULT 21

ABR62392
 ID ABR62392 standard; protein; 602 AA.

ABR62392;

03-OCT-2003 (first entry)

Human butyrylcholinesterase.

Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;

EC-3.1.1.8.

Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..18

FT Protein /label= signal peptide

FT Protein /label= Butyrylcholinesterase

PN MO2003054182-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002MO-IB005526.

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XX 21-DEC-2001; 2001US-0344295P.
PR (NEXT-) NEXIA BIOTECHNOLOGIES INC.
PA Karatzas C, Huang Y, Lazaris A;
PI WPI; 2003-559148/52.
XX N-PSDB; ACC641170.
DR
XX New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase
PT (BChE) enzyme in its milk or urine, useful for large-scale production of
PT recombinant BChE to prevent or treat organophosphate poisoning or cocaine
PT intoxication.
XX
PS Disclosure; Fig 1A; 112pp; English.
XX
XX The present sequence is the protein sequence of human
CC butyrylcholinesterase (BChE), including the native signal peptide which
CC is cleaved during processing to produce the mature BChE protein. The
CC invention provides methods for large-scale production of recombinant BChE
CC in cell culture, and in the milk and/or urine of transgenic mammals. The
CC genome of the transgenic mammal (e.g. goat) comprises a DNA sequence that
CC encodes BChE operably linked to a mammary gland-specific promoter or to a
CC urinary endothelium-specific promoter, and a signal sequence that
CC provides secretion of the BChE enzyme into the milk or urine of the
CC mammal. The recombinant BChE can be used in preventing and/or treating
CC organophosphate pesticide poisoning, nerve gas poisoning, cocaine
CC intoxication or succinylcholine-induced apnoea
XX
SQ Sequence 602 AA;
Query Match 99.5%; Score 3096; DB 6; Length 602;
Best Local Similarity 99.8%; Pred. No. 4.7e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRLRKKKQSLTKMSDINWATK 60
DB 29 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRLRKKKQSLTKMSDINWATK 88
QY 61 YANSCCONIDQSPFGHSGEMNPNTDLSBDCYLVNWIPAPKRNATVLIWYGGGFQT 120
DB 89 YANSCCONIDQSPFGHSGEMNPNTDLSBDCYLVNWIPAPKRNATVLIWYGGGFQT 148
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLFPOQLALQWVK 180
DB 149 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLFPOQLALQWVK 208
QY 181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHLFTRAIILOSGSFNAPWATVSLYEAR 240
DB 209 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHLFTRAIILOSGSFNAPWATVSLYEAR 268
QY 241 NRTINLAKLTGCSRENTEIITKLRNKPDEIILNFAFVVPYGTPLSVNFGPTVDGFLT 300
DB 269 NRTINLAKLTGCSRENTEIITKLRNKPDEIILNFAFVVPYGTPLSVNFGPTVDGFLT 328
QY 301 DMPDIIIEGQFKKTQILVGNKDEGTWFLVYGAPEGSKONNSIITRKEFOEGIKTFPPG 360
DB 329 DMPDIIIEGQFKKTQILVGNKDEGTWFLVYGAPEGSKONNSIITRKEFOEGIKTFPPG 388
QY 361 VSEBGEKSLIFHYTDWDDORPENYREALGDVVDYNIICPALFTFKKFSWGNNAFFYY 420
DB 389 VSEBGEKSLIFHYTDWDDORPENYREALGDVVDYNIICPALFTFKKFSWGNNAFFYY 448
QY 421 FEHRSSKLPWPEWGVHGEIEFVFGILPERRDNYTKAEIILSRSLYKMANPAKYNP 480
DB 449 FEHRSSKLPWPEWGVHGEIEFVFGILPERRDNYTKAEIILSRSLYKMANPAKYNP 508
QY 481 NETONNSGWFVPESTOKYTLTNTSESTRIMTKLRAOCCRFMTSPFPVLEMTGNIDBAE 540
DB 509 NETONNSGWFVPESTOKYTLTNTSESTRIMTKLRAOCCRFMTSPFPVLEMTGNIDBAE 568
QY 541 WEMKAGFHRNNYMMDMKNQGFNDYTSKKSCVGL 574

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DB 569 WEMKAGFHRNNYMMDMKNQGFNDYTSKKSCVGL 602
|||||
RESULT 22
ADFP90908
ID ADF90908 standard; protein; 602 AA.
XX
XX ADF90908;
AC
XX 26-FEB-2004 (first entry)
DE Human hepatic-fibrosis disease marker protein SEQ ID 370.
XX
XX Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
KW hepatic carcinoma; human.
XX
OS Homo sapiens.
XX
XX JP2003259877-A.
PN
XX 16-SEP-2003.
PD
XX 11-MAR-2002; 2002JP-00065013.
PF
XX 11-MAR-2002; 2002JP-00065013.
PR
XX (SUMU ) SUMITOMO SEIYAKU KK.
PA
XX WPI; 2003-821598/77.
DR
XX Hepatic fibrosis disease markers comprising polynucleotides or
PT antibodies, useful for improved diagnosis, screening and developing drugs
PT to treat hepatitis, to control cirrhosis and carcinoma.
XX
XX Claim 3; SEQ ID NO 370; 313pp; Japanese.
XX
XX The present invention relates to hepatic-fibrosis disease markers
CC (ADFP90539-ADFP90871) and related proteins (ADFP90872-ADFP90917). The
CC sequences are useful for detecting and treating hepatic fibrosis caused
CC by alcohol consumption, virus infection, etc., and the associated chronic
CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
CC precision), so more suitable treatments can be developed and given.
XX
SQ Sequence 602 AA;
Query Match 99.5%; Score 3096; DB 7; Length 602;
Best Local Similarity 99.8%; Pred. No. 4.7e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRLRKKKQSLTKMSDINWATK 60
DB 29 EDDIIITATKNGKRGKGNLTVFGGTVAFLGIPYAPPLGRLRKKKQSLTKMSDINWATK 88
QY 61 YANSCCONIDQSPFGHSGEMNPNTDLSBDCYLVNWIPAPKRNATVLIWYGGGFQT 120
DB 89 YANSCCONIDQSPFGHSGEMNPNTDLSBDCYLVNWIPAPKRNATVLIWYGGGFQT 148
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLFPOQLALQWVK 180
DB 149 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNBPAPGNMGLFPOQLALQWVK 208
QY 181 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHLFTRAIILOSGSFNAPWATVSLYEAR 240
DB 209 NIAAFGNPKSVTLFGESAGAAVSLSLSPGSHLFTRAIILOSGSFNAPWATVSLYEAR 268
QY 241 NRTINLAKLTGCSRENTEIITKLRNKPDEIILNFAFVVPYGTPLSVNFGPTVDGFLT 300
DB 269 NRTINLAKLTGCSRENTEIITKLRNKPDEIILNFAFVVPYGTPLSVNFGPTVDGFLT 328
QY 301 DMPDIIIEGQFKKTQILVGNKDEGTWFLVYGAPEGSKONNSIITRKEFOEGIKTFPPG 360

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Db 329 DMPDILLELGQFKKTQILVGNKDEGTAFVYGAPEGSKDNNSITTRKEFOEGKIFPPG 388
 Qy 361 VSEFGKESILFHYTDWDQDRPENYREALGDVGVNFCALPFTKKFSWMGNNAFFYY 420
 Db 369 VSEFGKESILFHYTDWDQDRPENYREALGDVGVNFCALPFTKKFSWMGNNAFFYY 448
 Qy 421 FEHRSSKLPWPEWGMVGHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480
 Db 449 FEHRSSKLPWPEWGMVGHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 508
 Qy 481 NETQNNSTSWPVFKSTQKYLTLNTESRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540
 Db 509 NETQNNSTSWPVFKSTQKYLTLNTESRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 568
 Qy 541 MEWKAGFHRNNNTMMDKNQFNNDYTSKESCVGL 574
 Db 569 MEWKAGFHRNNNTMMDKNQFNNDYTSKESCVGL 602

RESULT 23

ID ADR01045 standard; protein; 574 AA.
 XX ADR01045;

DT 23-SEP-2004 (first entry)
 DE Butyrylcholinesterase A328W/S287G/F227A/A199S variant.

KM butyrylcholinesterase; cocaine-induced condition;
 KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
 KM cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.
 OS Synthetic.

PN US2004121970-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

PR 20-DEC-2002; 2002US-00324466.

PA (WATK/) WATKINS J D.
 PA (PANC/) PANCOOK J D.

PI Watkins JD, Pancook JD;

XX WPI; 2004-468195/44.
 DR N-PSDB; ADR01044.

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
 PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
 XX

PS Claim 1; SEQ ID NO 12; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)
 CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
 CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
 CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
 CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
 CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
 CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
 CC polypeptide comprising any of the 21 sequences of 57 amino acids each
 CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
 CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
 CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
 CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
 CC cocaine addiction. This is the amino acid sequence of a human
 CC butyrylcholinesterase variant.

XX Sequence 574 AA;
XX

Query Match 99.5%; Score 3095; DB 8; Length 574;
 Best Local Similarity 99.5%; Pred. No. 5,4e-277;
 Matches 571; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDDIIITKNGKVRGNALTYFGGTATFLGIPYAOPLGLRFRKPKPSLTKWSIMWATK 60
 Db 1 EDDIIITKNGKVRGNALTYFGGTATFLGIPYAOPLGLRFRKPKPSLTKWSIMWATK 60
 Qy 61 YANSCCNIDQSPFGFGSEMMNPNTDLSBDCILYANWIPAPKXATVLIWYGGGFOF 120
 Db 61 YANSCCNIDQSPFGFGSEMMNPNTDLSBDCILYANWIPAPKXATVLIWYGGGFOF 120
 Qy 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNEAPAGNMGLPQOALALQWVK 180
 Db 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLGFALPGNEAPAGNMGLPQOALALQWVK 180
 Qy 181 NIAAFGNPKSVTLFGSSAGAASVSLHLSPGSHSLFTRAILQSGSFNAWATVSLYEAR 240
 Db 181 NIAAFGNPKSVTLFGSSAGAASVSLHLSPGSHSLFTRAILQSGSFNAWATVSLYEAR 240
 Qy 241 NRTLNLAKLTGCSRENETELIKLRNKPQELINLEAFVVPYGTPLGVNFGPTVDGFLT 300
 Db 241 NRTLNLAKLTGCSRENETELIKLRNKPQELINLEAFVVPYGTPLGVNFGPTVDGFLT 300
 Qy 301 DMPDILLELGQFKKTQILVGNKDEGTAFVYGAPEGSKDNNSITTRKEFOEGKIFPPG 360
 Db 301 DMPDILLELGQFKKTQILVGNKDEGTAFVYGAPEGSKDNNSITTRKEFOEGKIFPPG 360
 Qy 361 VSEFGKESILFHYTDWDQDRPENYREALGDVGVNFCALPFTKKFSWMGNNAFFYY 420
 Db 361 VSEFGKESILFHYTDWDQDRPENYREALGDVGVNFCALPFTKKFSWMGNNAFFYY 420
 Qy 421 FEHRSSKLPWPEWGMVGHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480
 Db 421 FEHRSSKLPWPEWGMVGHGVEIEFVFGPLERRDNYTKAEIISRSIVKRWANPAKYGNP 480
 Qy 481 NETQNNSTSWPVFKSTQKYLTLNTESRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540
 Db 481 NETQNNSTSWPVFKSTQKYLTLNTESRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540
 Qy 541 MEWKAGFHRNNNTMMDKNQFNNDYTSKESCVGL 574
 Db 541 MEWKAGFHRNNNTMMDKNQFNNDYTSKESCVGL 574

RESULT 24

ID ADR01059 standard; protein; 574 AA.
 XX ADR01059;

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase V331L variant.

KM butyrylcholinesterase; cocaine-induced condition;
 KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
 KM cocaine addiction; human; butyrylcholinesterase variant.

OS Homo sapiens.
 OS Synthetic.

PN US2004121970-A1.

PD 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

PR 20-DEC-2002; 2002US-00324466.

PA (WATK/) WATKINS J D.
 PA (PANC/) PANCOOK J D.

XX Watkins JD, Pancook JD;
PI ADR01075
XX WPI, 2004-468195/44.
DR N-PSDB; ADR01058.
XX

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
XX Claim 1, SEQ ID NO 26; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX

XX Sequence 574 AA:

Query Match 99.5%; Score 3093; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 8.3e-277;
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKKGKRGKGNLTVFGGTVAFLGIPYAPPLGRLPKKQSLTKMSDINWATK 60
DB 1 EDDIIATKKGKRGKGNLTVFGGTVAFLGIPYAPPLGRLPKKQSLTKMSDINWATK 60
QY 61 YANSCCNIDQSPFGHSEMMNPNTDLSBDCLYLWVWIPAPKKNATVLIWYGGGFQT 120
DB 61 YANSCCNIDQSPFGHSEMMNPNTDLSBDCLYLWVWIPAPKKNATVLIWYGGGFQT 120
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLFGALPGNPPAPGNMGLFPOQLALQWVK 180
DB 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLFGALPGNPPAPGNMGLFPOQLALQWVK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTRALILOGSFNAPWATSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTRALILOGSFNAPWATSLYEAR 240
QY 241 NRTLNLAKTGCSRENETEIKCLRNDPQEIILNEAFVVPYGTPLSVNFGPTVDGDFLT 300
DB 241 NRTLNLAKTGCSRENETEIKCLRNDPQEIILNEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILLGLGPKTKTQIILVGNKDEGTMFLVYGAPGSKNNSITTRKEPQEGKIFPPG 360
DB 301 DMPDILLGLGPKTKTQIILVGNKDEGTMFLVYGAPGSKNNSITTRKEPQEGKIFPPG 360
QY 361 VSEFGKESILFHYTDWDDORPENYREALGVVDYVFCALFETKFSWGNNAFFYY 420
DB 361 VSEFGKESILFHYTDWDDORPENYREALGVVDYVFCALFETKFSWGNNAFFYY 420
QY 421 FEHSSSKLPWDEWGVHGYEIEFVFGPLERRDNYTAAEILSRSIYKMANFATKGNP 480
DB 421 FEHSSSKLPWDEWGVHGYEIEFVFGPLERRDNYTAAEILSRSIYKMANFATKGNP 480
QY 481 NETQNNSTSWPEVSTKQKYLTLNTESTRIMTKLRAOCCRFWTSFPFVLEMTGNIDAE 540
DB 481 NETQNNSTSWPEVSTKQKYLTLNTESTRIMTKLRAOCCRFWTSFPFVLEMTGNIDAE 540
QY 541 WEMKAGFHRNNMYMDKNOFNDYTSKKSCYGL 574
DB 541 WEMKAGFHRNNMYMDKNOFNDYTSKKSCYGL 574

RESULT 25
ADRO1075
ID ADR01075 standard; protein; 574 AA.
XX
XX ADR01075;
AC

DT 23-SEP-2004 (first entry)
XX
XX Human butyrylcholinesterase A199S variant.
DE

XX butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX

OS Homo sapiens.
OS Synthetic.
XX

PN US2004121970-A1.
XX

PD 24-JUN-2004.
XX

PF 20-DEC-2002; 2002US-00324466.
XX

PR 20-DEC-2002; 2002US-00324466.
XX

PA (WATK/) WATKINS J D.
PA (PANC/) PANCOCK J D.
XX

PI Watkins JD, Pancook JD;
XX

XX WPI, 2004-468195/44.
DR N-PSDB; ADR01074.
XX

PT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX

XX Claim 1, SEQ ID NO 42; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX

XX Sequence 574 AA:

Query Match 99.5%; Score 3093; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 8.3e-277;
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKKGKRGKGNLTVFGGTVAFLGIPYAPPLGRLPKKQSLTKMSDINWATK 60
DB 1 EDDIIATKKGKRGKGNLTVFGGTVAFLGIPYAPPLGRLPKKQSLTKMSDINWATK 60
QY 61 YANSCCNIDQSPFGHSEMMNPNTDLSBDCLYLWVWIPAPKKNATVLIWYGGGFQT 120
DB 61 YANSCCNIDQSPFGHSEMMNPNTDLSBDCLYLWVWIPAPKKNATVLIWYGGGFQT 120
QY 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLFGALPGNPPAPGNMGLFPOQLALQWVK 180
DB 121 GTSSLHYDQKFLARVERVIVSMNRYVAGLFGALPGNPPAPGNMGLFPOQLALQWVK 180
QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTRALILOGSFNAPWATSLYEAR 240
DB 181 NIAAFGNPKSVTLFGESAGAASVSLHLSPGSHLFTRALILOGSFNAPWATSLYEAR 240

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Db 181 NIAFGGNPKSVTLFGSSGAASVSIHLSPGSHSLFTRAILQSGSFNAPMAVTSIYEAR 240
Qy 241 NRTLNIAKLTCGSRNETETIICKLRNKDPOEILNBAFVVPYGTPLSVNFGPTVDGDEL 300
Db 241 NRTLNIAKLTCGSRNETETIICKLRNKDPOEILNBAFVVPYGTPLSVNFGPTVDGDEL 300
Qy 301 DMPDILLELGQFKKTQILVGVNDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLELGQFKKTQILVGVNDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Qy 361 VSEFGKESILFHYTDWDDQRPENYRALGDVVDYVNFICPALEFTKKFSKGNNAFFYY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYRALGDVVDYVNFICPALEFTKKFSKGNNAFFYY 420
Qy 421 FEHRSKLPMPWEMGVHGYEIEFVFGPLERDNTYKAEIILSRSIYKRWANPAKYGNP 480
Db 421 FEHRSKLPMPWEMGVHGYEIEFVFGPLERDNTYKAEIILSRSIYKRWANPAKYGNP 480
Qy 481 NETQNNSTSWPVFKSTEQKTLTNTTESTRIMTKLRQAQCRFWTSFPPKVLMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKTLTNTTESTRIMTKLRQAQCRFWTSFPPKVLMTGNIDEAE 540
Qy 541 WEWKAGFHRNNYMMDMKQNDYTSKESCVGL 574
Db 541 WEWKAGFHRNNYMMDMKQNDYTSKESCVGL 574
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Job time : 164 secs

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